

TITLE MLO-genes controlling diseases
JOURNAL Patent: WO 0078799-A 5 28-DEC-2000;
Novartis AG (CH)
FEATURES
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Best Local Similarity 99.6%; Pred. No. 8.1e-297;
Matches 1687; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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ACCESSION	AX063294		
VERSION	AX063294.1	GI:12541084	
KEYWORDS			
SOURCE	Triticum sp.		
ORGANISM	Triticum sp. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum. 1 (bases 1 to 1868) Salmeron,J.M., Weislo,L.J., Strawn,L.J., Kramer,C.M., Wang,H.X., Vernooij,B.T., Levin,J.Z., Helletz,P.B., Patton,D.A. and Que,Q. Mn-genes controlling diseases Patent: WO 0078799-A 3 28-DEC-2000; Novartis AG (CH)		
FEATURES	Location/Qualifiers		
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LOCUS AF84145
DEFINITION Triticum aestivum M101 protein mRNA, complete cds.
ACCESSION AF84145
VERSION AF84145.1 GI:14334168
KEYWORDS
SOURCE Triticum aestivum.
ORGANISM Triticum aestivum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
AUTHORS Yu, L., Niu, J., S., Ma, Z., Q., Chen, P., D., and Liu, D., J.
TITLE Cloning, characterization analysis and expression of M101 gene from
wheat
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1721)
AUTHORS Yu, L., Niu, J., S., Ma, Z., Q., Chen, P., D., and Liu, D., J.
TITLE Direct Submission

JOURNAL Submitted (23-MAY-2001) Key Laboratory of Crop Cytogenetics,
Nanjing Agricultural University, Nanjing, Jiangsu, China
FEATURES
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Best Local Similarity 96.98; Pred. No. 4.2e-278;
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Db	1497	AGCGCAACTGCGCGCAAGGCGCATGAGAGGCGTATGATCCCGGTTGTGTGGGG	1556
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Qy	1561	GATGCGCATGCCAGGCGAGATTTTTCCTTCAGGCGGAGTGAAGCAAGTTATGAT	1620
Db	1617	GATGCGCATGCCAGGCGAGATTTTTCCTTCAGGCGGAGTGAAGCAAGTTATGAT	1676
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Db	1677	TGATGTTAGTCCATGTAATGACCAACATGATGATGATGATTCGT	1721

RESULT 5
AX063298
LOCUS AX063298 1886 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 7 from Patent WO07879.
ACCESSION AX063298

VERSION	AX063298.1	GI:12541088
KEYWORDS		
SOURCE	Triticum sp.	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
REFERENCE	1 (bases 1 to 1886)	
AUTHORS	Salmeron, J. M., Weisio, L. J., Strawn, L. J., Kramer, C. M., Wang, H. X., Vernon, J. B., Levin, J. Z., Heifetz, P. B., Patton, D. A. and Que, Q.	
TITLE	Mio-genes controlling diseases	
JOURNAL	Patent: WO 0078799-A 7 28-DEC-2000;	
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Matches 1615; Conservative	0; Mismatches 74; Inels 0; Gaps 0;	
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Db	258	GTGGCGCTGCTTCCCGCTCATGATCATGCTGTCCTCCTCGGAGACGCGCTCCAC 317
Qy	121	AAGTCGGCCATTGGTTCACCAAGGCGACAAAGCGCGTGGCGGAGGCGCTGGAAAG 180
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Qy	181	ATCAAAAGCGAGCTGATGCTGTGGGTTTCATCTGCTGCTGCTGCTGCTGCTGCTG 240
Db	378	ATGAAGCGGAGCTGATGCTGTGGGTTTCATCTGCTGCTGCTGCTGCTGCTGCTG 437
Qy	241	CCATTCCTCGGATATGATCTTCGAGAAAGGCGCCGACGATCATGCGGCGCTGACGCTG 300
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Qy	301	CCCCCTGTTCCGTCAGAGCAAGTACAAAGACTACTAGTGGCCCAAAAGAGGCAAGGTG 360
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Qy	361	TGCGTATATGTCACAGGCGAGCTTGACACAGCTCCACATATATCTTGTGCTGCGCGTC 420
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RESULT 6
AF384144 1819 bp mRNA linear PLN 10-JUN-2001
LOCUS AF384144
DEFINITION Trilicium aestivum MLO protein mRNA, complete cds.
ACCESSION AF384144
VERSION AF384144.1 GI:14334166
KEYWORDS
SOURCE
ORGANISM
Trilicium aestivum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triliceae; Trilicium.
REFERENCE
Yu, L., Niu, J.-S., Ma, Z.-Q., Chen, P.-D. and Liu, D.-J.
1 (bases 1 to 1819)
Cloning, location and expression of MLO gene from wheat
Unpublished
2 (bases 1 to 1819)
Yu, L., Niu, J.-S., Ma, Z.-Q., Chen, P.-D. and Liu, D.-J.
Direct Submission
AUTHORS
TITLE
JOURNAL
Nanjing Agricultural University, Nanjing, Jiangsu, China
location/Qualifiers
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BASE COUNT 374 a 552 c 525 g 368 t
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Best Local Similarity 95.5%; Pred. No. 1.6e-263;
Matches 1545; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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Qy	661	TTCCATACCTTGAGGGGCAAGGTTATCAACAGCGGCAATTTGTTCGATATCAACGAAATGTGAC	720
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Qy	841	CTTACCTTGATTTCTTTCATCCCTCTCTGTTCATCTCTTGTGTGTGTGGAACCAAGCTGAG	900
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Qy	1441	GGCGCGACCTCGCCAAAGGACCATGTGAGAGGCTAGGGACATGACCCGGTGTGTGTGGCG	1500
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Qy	1561	GATGCCGACATCCCGACCGCAGATTTTTCCTTCAGCCAGGATGAGACAAATTTATG	1617
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RESULT 7			
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DEFINITION	Sequence 7 from Patent WO9804586.		linear
ACCESSION	A92833		
VERSION	A92833.1	GI:6741370	
KEYWORDS			
SOURCE	Hordeum vulgare.		
ORGANISM	Hordeum vulgare.		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	Pooidae; Trilicaceae; Hordeum.		
	1 (bases 1 to 1917)		
REFERENCE	Panstruga,R. and Bueschges,R.		
AUTHORS	POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN		
TITLE	PLANTS		
JOURNAL	Patent: WO 9804586-A 7 05-FEB-1998;		
	INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)		
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Query Match	81.1%; Score 1387.8; DB 6; Length 1917;		
Best Local Similarity	90.0%; Pred.No. 8.9e-243;		
Matches 1522; Conservative	0; Mismatches 162; Indels 7; Gaps 3;		
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Db	69	CGCTTCGCGCTCATGATCATGTGTGTCGCTCTCTCTGAGAACAGCGGCTCCCAAGCTCGG	128
Qy	290	GGTCTTCGCGCGCTCATGATCATGTGTGTCGCTCTCTCTGAGAACAGGCTTCCAAGCTCGG	349
Db	129	CCATTGGTTCACAGACCGGACAAAGAGGCCCTGTGGAGCGCTGTGAAGATGAAGCTC	409
Qy	350	CCATTGGTTCACAGACCGGACAAAGAGGCCCTGTGGAGCGCTGTGAAGATGAAGCTC	469
Db	189	GAGAGTACGCTGTGGGGTTTATCTGCTGCTCTCTGCGGTGACGACAGAGACC--AAT	245
Qy	410	GGAGCTCATGCTGGGGTTTATCTGCTGCTCTCTATCTGATGACGACAGACCCATCAT	469

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OY	306	TGGTCCGTCAGAGCAAGTACAAAGACTACTCTCGCCGCAAAAAGGCAAGGTGCGT	365
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OY	426	TGTCACTACAGCGTCTATCATATGCTCTTAAGCCGCTCAAAATGAGACATGAGAAG	485
Db	647	TGTCACTACAGCGTCTATCATATGCTCTTAAGCCGCTCAAAATGAGAACATGAGAAG	706
OY	486	ATGGAGACAGAGACCGGCTCTTGGATACAGTTCGCAATGATCTCGCGGTTCGG	545
Db	707	ATGGAGACAGAGACCGCTCTTGGATACAGTTCGCAATGATCTCGCGGTTCGG	766
OY	546	CTTCACGACACAGAGGTGTCGTGAAGGGGACCGTGGGCTCTCCAGACCCCGGCAAT	605
Db	767	GTTCCAGCAACAGAGGTGTCGTGAAGGGGACCGTGGGCTCTCCAGACCCCGGCAAT	826
OY	606	CAATAGGTGTGTGCGCTTCTTCAGGCAAGTCTTCAGTGTGTCACCAAGGTGACTACT	665
Db	827	CAGATGTGTGTGCGCTTCTTCAGGCAAGTCTTCAGTGTGTCACCAAGGTGACTACT	886
OY	666	CACCTGAGGGGAGGCTTCATCAACGGGCGATTTGTGCGATAACAGCAAGTTCACATCCA	725
Db	887	GACCTGAGGGGAGGCTTCATCAACGGGCGATTTGTGCGATAACAGCAAGTTCACATCCA	946
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Db	947	CAAGTCAATCAAGAGGTGCATATGAGAGCAAGCTTCAAGTCCGTGGCATCAGCCTCCC	1006
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Db	1007	GCTGTGCTGTGGCGATCTCAACCTCTTCTTGATATGACGGGATCGGACGCTCAC	1066
OY	846	CTGGAATTTTTCATCCCTTCGTCATCCCTTGTCATCCCTTGTCGTAAGTCGAGATGAT	905
Db	1067	CTGGAATTTTTCATCCCTTCGTCATCCCTTGTCATCCCTTGTCGTAAGTCGAGATGAT	1126
OY	906	CATCATGAGAGAGGCCCTCGAGATCCAGAGACCGGGCAGAGCTCATCAAGGGGCGCCGT	965
Db	1127	CATCATGAGAGAGGCCCTCGAGATCCAGAGACCGGGCAGAGCTCATCAAGGGGCGCCGT	1186
OY	966	GTTTGAAGCCCAACAAGTCTTGTGTTCACCGCCGCCACATCGGGTCCCTCTTCTCAT	1025
Db	1187	GTTTGAAGCCCAACAAGTCTTGTGTTCACCGCCGCCACATCGGGTCCCTCTTCTCAT	1246
OY	1026	ACACCTGAGAGCGTTCGAGATGGGTTTCAGATGGGACATTTGCTGTGACATGAGCCAC	1085
Db	1247	ACACCTGAGAGCGTTCGAGATGGGTTTCAGATGGGACATTTGCTGTGACATGAGCCAC	1306
OY	1086	GCCCGGCTTGAAGAAATGCTTCCATATGCAATCGGTGAGCATCATGAAAGGTCGTGCT	1145
Db	1307	GCCCGGCTTGAAGAAATGCTTCCATATGCAATCGGTGAGCATCATGAAAGGTCGTGCT	1366
OY	1146	GGGGCTGTGCTTCAGTTCCTGTGACGCTATATACATCTCCCGCTACAGCGCTGTGAC	1205
Db	1367	GGGGCTGTGCTTCAGTTCCTGTGACGCTATATACATCTCCCGCTACAGCGCTGTGAC	1426
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Db	1487	CAACTGCGGGAACACGGCCAGAGAGGAAGAGGTTCGAGACACGGACATGCTGATGGC	1546

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QY 1685 TTTACGATGATC 1695

Db 1907 TTTACGATGATC 1917

LOCUS	HYMLO	1917 bp	mRNA	linear	PLN 07-MAR-1997
DEFINITION	H vulgare mRNA for MLO protein.				
ACCESSION	Z83834				
VERSION	Z83834.1 GI:1877220				
KEYWORDS	MLO gene.				
SOURCE	Hordeum vulgare subsp. vulgare.				
ORGANISM	Hordeum vulgare subsp. vulgare				
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillipsoida; Poales; Poaceae;				
AUTHORS	Pooladee, Triticaceae; Hordeum.				
	1 (bases 1 to 1917)				
	Bueschges, R., Hollricher, K., Panstruga, R., Simons, G., Wolter, M.,				
	Fritsch, A., van Daelen, S., Vos, P., Diergaarde, P.,				
	Groenendijk, J., Joepsch, S., Vos, P., Salmalm, F. and				
	Schulze-Lepert, P.				
TITLE	The barley MLO gene: a novel control element of plant pathogen resistance				
JOURNAL	Cell 88 (5), 695-705 (1997)				
MEDLINE	97207016				
PUBMED	9054509				
REFERENCE	2 (bases 1 to 1917)				
AUTHORS	Panstruga, R.				
JOURNAL	Direct Submission				
	Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury				
	Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK				
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ORIGIN

Query Match 81.1%; Score 1387.8; DB 8; Length 1917;
Best Local Similarity 90.0%; Pred. No. 8.9e-243;
Matches 1522; Conservative 0; Mismatches 162; Indels 7; Gaps 3;

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RESULT 9
A92828 LOCUS A92828 1602 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 2 from Patent WO9804386.
ACCESSION A92828

VERSION A92828.1 GI:6741365
KEYWORDS
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 1602)
AUTHORS Panstruga, R. and Bueschges, R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
PLANTS
JOURNAL Patent: WO 9804586-A 2 05-FEB-1999;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
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AF361933
LOCUS AF361933
DEFINITION
Triticum aestivum seven transmembrane-spanning protein (MLO) mRNA,
partial cds.
ACCESSION AF361933
VERSION AF361933.1 GI:15290590
KEYWORDS
SOURCE Triticum aestivum.
ORGANISM Triticum aestivum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 1399)
AUTHORS Devoto, A., Hartmann, A., Piffenelli, P., Elliott, C., Simons, C.,
Taramino, G., Goh, C.-S., Schulze-Lefert, P., and Panstruga, R.
TITLE Co-Evolution among intracellular domains and the C-terminus of the
seven-transmembrane Mlo protein is suggested by a detailed
computational analysis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1399)
AUTHORS Elliott, C.E. and Schulze-Lefert, P.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2001) The Sainsbury Laboratory, John Innes
Center, Colney Lane, Norwich NR4 7UH, UK
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DEFINITION Sequence 12 from Patent WO9804586.
ACCESSION A92838
VERSION A92838.1 GI:6741374
KEYWORDS Hordeum vulgare.

ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1635)
AUTHORS Panstruga, R. and Bueschges, R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN PLANTS
JOURNAL Patent: WO 9804586-A 12 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRU GA RALPH (GB)
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/clone="MLO HOMOLOGUE"
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Query Match 56.28; Score 962.2; DB 6; Length 1635;
Best Local Similarity 76.88; Pred. No. 2.8e-165;
Matches 1267; Conservative 0; Mismatches 268; Indels 114; Gaps 3;
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RESULT 12
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DEFINITION Oryza sativa seven transmembrane protein MLO2 mRNA, complete cds.
ACCESSION AF384030
VERSION AF384030.1 GI:15290604
KEYWORDS
SOURCE Oryza sativa (indica cultivar-group).
ORGANISM Oryza sativa (indica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS

Ehrhardtideae; Oryzeae; Oryza.
1 (bases 1 to 1740)
Devoto, A., Hartmann, H. A., Piffanel, P., Elliott, C., Simmons, C.,
Taramino, G., Goh, C.-S., Cohen, F. E., Schulze-Lefert, P. and
Panstruga, R.

TITLE

Molecular phylogeny and domain-specific co-evolution of the
plant-specific seven transmembrane MLO family

JOURNAL
REFERENCE

2 (bases 1 to 1740)
Elliott, C. and Schulze-Lefert, P.

AUTHORS

Direct Submission
Submitted (22-MAY-2001) The Sainsbury Laboratory, Colney Lane,
Norwich NR4 7QH, UK

JOURNAL
TITLE

Location/Qualifiers

FEATURES

source

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BASE COUNT
ORIGIN

396 a 446 c 534 g 364 t

Query Match

51.4%; Score 879.6; DB 8; Length 1740;

Best Local Similarity

73.5%; Pred. No. 3e-150; Mismatches 324; Indels 117; Gaps 3;

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Qy 87 CATCGTCTGCTCTCTCTGAGCAGCGCTCCACAAGCTCGCCATTGGTCCACAAGCG 146
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Qy 666 CACCTGAGGAGGAGGCTTCATCAAGCGGATGATGATGATGATGATGATGATGAT 725
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DEFINITION	AF388195	1894 bp	mRNA	linear
ACCESSION	Oryza sativa M10 (M10)	mRNA, complete cds.		
VERSION	AF388195.1	GI:14718603		
KEYWORDS				
SOURCE	Oryza sativa	(indica cultivar-group).		
ORGANISM	Oryza sativa	(indica cultivar-group).		

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 1894)	Kim, M.-C., Panstruga, R., Elliott, C., Muller, J., Devoto, A., Yoon, H.-W., Park, H.-C., Cho, M.-J., and Schuler-Scerif, P.	Calmodulin interacts with MLO protein to regulate defence against mildew in barley	Nature 416 (6879), 447-451 (2002)

REFERENCE	2 (bases 1 to 1894)
AUTHORS	Kim,M.C., Lee,S.H., Kim,J.K., Chun,H.J., Kim,J.C., Heo,W.D., Chung,W.S., Choi,M.S., Park,C.Y., Yoon,H.W. and Cho,M.U.
TITLE	Isolation and characterization of Mlo homolog in rice
JOURNAL	unpublished
REFERENCE	3 (bases 1 to 1894)
AUTHORS	Kim,M.C., Lee,S.H., Kim,J.K., Chun,H.J., Kim,J.C., Heo,W.D., Chung,W.S., Choi,M.S., Park,C.Y., Yoon,H.W. and Cho,M.U.
TITLE	Direct Submission
JOURNAL	Submitted (01-JUN-2001) Biochemistry, Gyeongsang National University, Gazwa-dong 900, Chinju 660-701, Korea
FEATURES	Location/Qualifiers
source	1. 1894

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Best Local Similarity	71.0%	Pred. No. 3.7e-142		
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QY	147	GCACAAAGAACGCGCTGGCGGAGGCGCTGGAGAAATCAAGAGGCGAGTATGCTGGTGGG	206
Db	279	GGAAAGAAAGAGCCATTTGGCGGAAAGGCTCTCGGGAAAGATCAAAAGCAGATTTGATGCTGCGGG	338
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Db	339	CTTCAATATGCTGTCTCTCACTGTGGACAAAGCGCCATCTCCAAAGATATGATCTCCCGGA	398
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RESULT 14
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DEFINITION Zea mays seven transmembrane protein Mlo1 mRNA, complete cds.
ACCESSION AY029312
VERSION AY029312.1 GI:13784974
KEYWORDS
SOURCE
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 1872)
TITLE Briggs, S.P. and Simmons, C.R.
JOURNAL Manipulation of mlo genes to enhance disease resistance in plants
2 (bases 1 to 1872) Patent: PCT WO/00/01722-B 07-JUL-1999;
REFERENCE
AUTHORS Cahoon, R.E., Miao, G.-H., Rafalski, J.A. and Taramino, G.
TITLE Zea mays cDNA encoding southern corn leaf blight resistance protein
JOURNAL Patent: PCT WO9923235-B 05-NOV-1999;
REFERENCE
AUTHORS Devoto, A., Hartmann, A., Piffanelli, P., Elliott, C., Simmons, C.R., Taramino, G., Goh, C.-S., Cohen, F.E., Schulze-Lefert, P. and Parastyrus, R.
TITLE Molecular phylogeny and domain-specific co-evolution of the plant-specific seven transmembrane Mlo family
JOURNAL Unpublished
REFERENCE
AUTHORS 4 (bases 1 to 1872)
TITLE Simmons, C.R., Taramino, G. and Powell, W.
JOURNAL Direct Submission
Submitted (06-APR-2001) Bioinformatics Department, Pioneer, A
DuPont Company, 7250 N.W. 62nd Avenue, Emerson, Box 552, Johnston,
IA 50131, USA

FEATURES
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BASE COUNT 394 a 560 c 554 g 364 t
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Db 1118 TGGTCTCTCTTCTTCATATACCTGACGAGCTCTTCAGAAATCGCTTCAGATGACATTT 1177
Oy 1068 CGTCTGACAGTGGCCAGCGCGCGCTTGAAGAAATGCTTCATATGACATGCGCTGAG 1127
Db 1178 CGTCTGACAGTGGCCAGCGCGCGCTTGAAGAAATGCTTCATATGACATGCGCTGAG 1236
Oy 1128 CATCATGAAGTCTGCTGTGGGCTGCTCTTCATGTTCTCTGACATATACCTTCC 1187
Db 1237 CATCATGAAGTCTGCTGTGGGCTGCTCTTCATGTTCTCTGACATATACCTTCC 1296
Oy 1188 CCTTACGCGCTGCTCACACAGATGGATGCAATGAAAGAGGTCATCTGTGAGAGGA 1247
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Oy 1365 GCCATGCTTAGCCCGGGCTTCTGACCGGTGACCTGCTTCCAAAGGCAATGGAGCTC 1424
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Oy 1605 A 1605
Db 1708 A 1708

RESULT 15
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LOCUS Sequence 11 from Patent WO9804586.
DEFINITION A92837
ACCESSION A92837
VERSION A92837.1 GI:6741373
KEYWORDS
SOURCE
ORGANISM
Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.
1 (bases 1 to 1611)
Panstruga, R. and Bueschges, R.
POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
PLANTS
Patent: WO 9804586-A 11 05-FEB-1998;
INNOS CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
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/clone="MLO HOMOLOGUE"
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ORIGIN
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Best Local Similarity 72.2%; Pred. No. 2,1e-132;
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Oy 89 TCGTCTCGCTCTCTCTGAGAGACGCGCTCCAGAGCTCGGCAATGTTCCAGAGCGC 148
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Oy 269 AGGCGCGACGATCATGGGCGCTGGAGCGCTGCGCCCTGCTGCTC---AAGAGCAATAC 327
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Oy 328 AAA-----GACTACTACTGCCCAAAAAG 352
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Oy 590 CCAGCACCCCGCATCATGATGGTGGGCTTCTTCAGGAGATTCCTCAGGATCGGTCA 649

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Db 734 GCAAGTTGACTCCCAAAATACATCAAGAGTCTTTGGAGCAGACTTCAAAGTGTG 793
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QY 1010 GGGTCTCTTCTTCATACCTGACGCTGTTCCAGAAATGCTTTCAGATGGCATTTCG 1069
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QY 1310 CGACATGCTGATGGCGCAGATGATCGGCGACGGCAGCCGAGGCGACGTGCCGA 1369
Db 1334 CGACGCGTCTGTGGCGCAGATGAGCGTGCAC-----TTCCGCGAGCCGG 1378
QY 1370 TGGCTAGCGGGGCTGTGACCGGTGACCTGCTTCA---CAAGGGCATGGAGCGTCCG 1426
Db 1379 GGTGAGCGGTGCGGCTGCGCGGTGACCTGCTGACAGTTCACAGGGCGGTGCGAGCC 1438
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Db 1559 CTTGTCGCGCGCATGCGCGA 1580
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Search completed: November 18, 2002, 14:03:23
Job time : 3096 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 12:11:37 ; Search time 263 Seconds

(without alignments)
14650.833 Million cell updates/sec

Title: US-09-857-896A-31

Perfect score: 1711

Sequence: 1 atggcggagagactacgagta.....agtcacaaaaaaaaaaaaa 1711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1711	100.0	21	AAAS2715
2	1684.6	98.5	22	AAAF24584
3	1683.6	98.4	20	AAZ30410
4	1616.2	94.5	20	AAZ30409
5	1616.2	94.5	22	AAAF24583
6	1570.6	91.8	20	AAZ30411
7	1570.6	91.8	22	AAAF24585
8	1386.2	81.0	19	AAV35026
9	1315.2	76.9	19	AAV35022

10	959	56.0	1635	19	AAV35020	Hordeum vulgare ML
11	780	45.6	1611	19	AAV35028	Oryza sativa MLO g
12	652.8	38.2	678	21	AAAS2707	Wheat MLO homologue
13	555.8	32.5	563	21	AAAS2704	Soybean MLO homolo
14	505.8	29.6	2425	19	AAV35025	Hordeum vulgare ML
15	425.6	24.9	2030	21	AAZ49561	Maize MLO2 protein
16	415.8	24.3	1815	21	AAZ49564	Maize MLO6 protein
17	415.8	24.3	1851	20	AAV35029	Zea mays SCLB pro
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20	359.2	21.0	2197	22	AAAF24586	Nucleotide sequenc
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22	300.4	17.6	1935	20	AAZ30413	Arabidopsis thalia
23	300.4	17.6	1935	22	AAAF24587	Nucleotide sequenc
24	300.4	17.6	2148	21	AAZ49560	Maize MLO3 cDNA
25	294.6	17.2	538	20	AAV35029	Zea mays SCLB pro
26	291.2	17.0	1782	20	AAZ30415	Arabidopsis thalia
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28	271.8	15.9	4105	19	AAV35029	Hordeum vulgare ML
29	261.6	15.3	1938	21	AAAS2705	Soybean MLO homolo
30	258.4	15.1	1666	21	AAAS2718	Wheat MLO homologue
31	254	14.8	1496	21	AAAS2708	Maize MLO3 cDNA
32	244.8	14.3	1869	21	AAZ50126	Maize monogenic di
33	244.8	14.3	1869	22	AAV35029	Maize MLO8 protein
34	237.4	13.9	1725	20	AAV35029	Maize MLO4 protein
35	237.4	13.9	1798	21	AAZ49566	Arabidopsis thalia
36	212	12.4	1745	21	AAV35023	Hordeum vulgare ML
37	210.6	12.3	2096	19	AAV35023	Nucleotide sequenc
38	210.2	12.3	1811	20	AAZ30414	Arabidopsis thalia
39	210.2	12.3	1811	22	AAAF24588	Nucleotide sequenc
40	210.2	12.3	1880	19	AAV35031	Maize MLO7 protein
41	191.4	11.2	1660	21	AAZ49565	Zea mays SCLB pro
42	171.6	10.0	1831	20	AAZ49562	Maize MLO4 protein
43	170	9.9	1841	21	AAZ49562	Soybean MLO homolo
44	158.6	9.3	960	21	AAV35023	Hordeum vulgare ML
45	154.8	9.0	513	21	AAV35022	Rice MLO homologue

ALIGNMENTS

RESULT 1	
ID	AAAS2715 standard; cDNA; 1711 BP.
XX	AAAS2715:
AC	27-OCF-2000 (first entry)
DT	
XX	Wheat MLO homologue putative coding sequence #4.
DE	
XX	Wheat; MLO homologue; disease resistance; ss.
KW	
XX	Triticum aestivum.
OS	
XX	Key
PH	Location/Qualifiers
FT	1..1605
FT	/tag= a
FT	/product= "MLO homologue"
XX	
XX	WO200036110-A2.
PD	
XX	22-JUN-2000.
XX	
XX	17-DEC-1999; 99WO-US30181.
XX	Nucleotide sequenc
PR	18-DEC-1998; 98US-0112737.
XX	
XX	(DUPO) DU POINT DE MEMOURS & CO E I.
PA	
XX	Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
PI	
XX	WPI; 2000-431590/37.

DR P-PSDB: AAB01805.

XX New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT creating transgenic plants with altered levels of disease resistance -
XX

PS Claim 2: Page 64: 79pp: English.

XX The present sequence is a putative coding sequence for a Mlo homologue
CC from wheat. It was identified by searching a root and leaf cDNA library
CC for sequences encoding proteins similar to Mlo from Hordeum vulgare
CC (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe
CC graminis f. sp. hordei upon the plant, and its inactivation leads to the
CC priming of disease resistance even if the pathogen is not present. The
CC gene and protein can be used to create transgenic plants which have
CC increased disease resistance, as well as allowing researchers to find
CC other resistance-conferring genes and proteins.

SQ Sequence 1711 BP: 377 A; 505 C; 473 G; 356 T; 0 other:

Query Match 100.0%; Score 1711; DB 21; Length 1711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 601 GGCATCAGATGGGTGTGGCTTCTTCAAGGAGTTCTTCAAGTGGTCAACAAGGTGAC 660
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DB 1081 GCCACGCGCGGCTTGAAGAAATGCTTCATATGACATCGGCTGACATCATGAAGTTC 1140
QY 1141 GTGCTGGGCTGGCTTTCAGATTCCTCTGAGCTATATACATTCCTCCCTCTACGCGCTC 1200
DB 1141 GTGCTGGGCTGGCTTTCAGATTCCTCTGAGCTATATACATTCCTCCCTCTACGCGCTC 1200
QY 1201 GTCCACAGATGGATGCAACATGAGAGGTGCTTTCGACAGAGAGGCGCAAGGCG 1260
DB 1201 GTCCACAGATGGATGCAACATGAGAGGTGCTTTCGACAGAGAGGCGCAAGGCG 1260
QY 1261 CTGACCAATGGCGGACACCGCCCAAGGAGAAAGAGTCCAGACAGGACATGCTG 1320
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DB 1321 ATGGCGCATATATGGGAGAGCGGACCGCCAGCGGAGAGTGGCGGATGCTTACGCTG 1380
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QY 1681 ATTTTCTAGTGAATAAAAA 1711
DB 1681 ATTTTCTAGTGAATAAAAA 1711

RESULT 2

AAF24584 standard: DNA: 1693 BP.

AAF24584:

DI 20-APR-2001 (first entry)
XX Nucleotide sequence of the wheat Mlo protein TrmLm2.
XX
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XX Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KM powdery mildew; Mlo; cell wall apposition; transgenic plant; sa.
XX
XX Triticum sp.
OS
FH
FH Key 1.1605 Location/Qualifiers
FT CDS
FT /tag= a
FT /product= "Mlo protein"
FT /transl_except= "(pos: 502..504, aa: Xaa)"
FT /note= "Xaa is an unspecified amino acid"
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XX M020007879-A2.
XX
XX 28-DEC-2000.
XX
XX 16-JUN-2000; 2000MO-EP05576.
XX
XX 18-JUN-1999; 9905-0336112.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERM GRS MBH.
XX
XX Salmeron JM, Welslo LJ, Strawn LJ, Kramer CM, Wang HX;
PI Vernool JF, Levin JZ, Helfetz PB, Patton DA, Que O;
XX
XX WPI: 2001-112311/12.
XX P-PSDB: AAB31251.
XX
XX Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT producing fungal resistant plants, in particular wheat plant -
XX
XX Claim 2; Page 92-94; 128pp; English.
XX
XX The present sequence encodes a Mlo protein. Mlo proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC Mlo proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC locus are responsible for a plant resistant pathotype. The mechanism
CC of Mlo resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding Mlo proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.
XX
XX Sequence 1693 BP; 360 A; 505 C; 472 G; 355 T; 1 other;
SQ
Query Match 98.5%; Score 1684.6; DB 22; Length 1693;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1687; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 1 ATGGGGAGAGTACAGTACCCCGCCGAGACCTCCCGAAGCCGCTCTGGGCG 60
DB 1 ATGGCGGAGAGTACAGTACCCCGCGGAGACCTCCCGAAGCCGCTCTGGGCG 60
OY 61 GTGGCGCTGCTTGGCGGATGATGATGCTCCGCTCTCTGAGACAGCGCTCCAC 120
DB 61 GTGGCGCTGCTTGGCGGATGATGATGCTCCGCTCTCTGAGACAGCGCTCCAC 120
OY 121 AAGCTGGCCATTGGTTCACAAAGCGGCAAGAAAGCGGCTGGGAGGCGCTGGAGAAG 180
DB 121 AAGCTGGCCATTGGTTCACAAAGCGGCAAGAAAGCGGCTGGGAGGCGCTGGAGAAG 180
OY 181 ATCAAGCGGAGCTGATGCTGTGGGGTTTCATCTCGCTGCTGCTGAGCAGAGAC 240
DB 181 ATCAAGCGGAGCTGATGCTGTGGGGTTTCATCTCGCTGCTGCTGAGCAGAGAC 240
OY 241 CCAATCTCGGATATGATCTCGAGAAGCGCGCAGATCATCGGCGCTGACGCTTG 300
DB 241 CCAATCTCGGATATGATCTCGAGAAGCGCGCAGATCATCGGCGCTGACGCTTG 300

DB 241 CCAATCTCGGATATGATCTCGAGAAGCGCGCAGATCATCGGCGCTGACGCTTG 300
OY 301 CCCCTGTTCGCTCAAGAGCAAGTACAAAGACTACTAGCGCCAAAGAGGCAAGGTG 360
DB 301 CCCCTGTTCGCTCAAGAGCAAGTACAAAGACTACTAGCGCCAAAGAGGCAAGGTG 360
OY 361 TCGCTAATGTCCAGGGGAGCTTGACACAGCTCCACATATTCATCTTCGCTCGCGTC 420
DB 361 TCGCTAATGTCCAGGGGAGCTTGACACAGCTCCACATATTCATCTTCGCTCGCGTC 420
OY 421 TTCATGTACACTACAGGCTCATCATCATGAGCTTAAGCGCTCAAAATGAGACATAG 480
DB 421 TTCATGTACACTACAGGCTCATCATCATGAGCTTAAGCGCTCAAAATGAGACATAG 480
OY 481 AAGAAATGGGAGACAGAGACCGGCTCTGGAAATACAGATTCCGAATGATCTCGCGCG 540
DB 481 AAGAAATGGGAGACAGAGACCGGCTCTGGAAATACAGATTCCGAATGATCTCGCGCG 540
OY 541 TTCGCTTCAGCACACAGAGCTGTCTGTAAGCGGCACCTGGGCTCTCCAGCACCCCG 600
DB 541 TTCGCTTCAGCACACAGAGCTGTCTGTAAGCGGCACCTGGGCTCTCCAGCACCCCG 600
OY 601 GGCATCAGATGGGTGGGTGGGCTCTTCAGGAGTTCCTCAGTGGCTCAGCAGGTGAC 660
DB 601 GGCATCAGATGGGTGGGTGGGCTCTTCAGGAGTTCCTCAGTGGCTCAGCAGGTGAC 660
OY 661 TACCTACCCCTGAGGGCAGGCTTCATCAACGGGCATTTGTGCATTAACAGAGTTGAC 720
DB 661 TACCTACCCCTGAGGGCAGGCTTCATCAACGGGCATTTGTGCATTAACAGAGTTGAC 720
OY 721 TTCCAAGTACATCAAGAGGTGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 TTCCAAGTACATCAAGAGGTGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
OY 781 CTCGCGCTGTGTGTGTGCGGATCTCACCTCTCTTGTATTTGAGGAGATCGGCAGC 840
DB 781 CTCGCGCTGTGTGTGTGCGGATCTCACCTCTCTTGTATTTGAGGAGATCGGCAGC 840
OY 841 CTCACCTGATTTTCTTCATCTCTCTGATCTCTCTGTGTGTGGAACCAAGCTGGAG 900
DB 841 CTCACCTGATTTTCTTCATCTCTCTGATCTCTCTGTGTGTGGAACCAAGCTGGAG 900
OY 901 ATGATCATCATGAGAGATGGCCCTGGAGATCCAGAGCCGGGAGCGTCAAGGGGGCG 960
DB 901 ATGATCATCATGAGAGATGGCCCTGGAGATCCAGAGCCGGGAGCGTCAAGGGGGCG 960
OY 961 CCCGTGTGAGCCACAGCAAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 961 CCCGTGTGAGCCACAGCAAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
OY 1021 TTCATACACCTGAGCGGTTCGCAAGTGGGTTTCAGATGAGCACTTTCGCTGAGACATG 1080
DB 1021 TTCATACACCTGAGCGGTTCGCAAGTGGGTTTCAGATGAGCACTTTCGCTGAGACATG 1080
OY 1081 GCCACGCCGCGTTGAAGAAATGCTTCATATGACATCGGTGTGAGCATATGAAGGTC 1140
DB 1081 GCCACGCCGCGTTGAAGAAATGCTTCATATGACATCGGTGTGAGCATATGAAGGTC 1140
OY 1141 GTGCTGGGGGTGGGCTCTTGTCTCTGAGGATATATACATCTCCCTCAAGCGCTC 1200
DB 1141 GTGCTGGGGGTGGGCTCTTGTCTCTGAGGATATATACATCTCCCTCAAGCGCTC 1200
OY 1201 GTACACAGATGGAGTGAACATGAAGAGTTCATCTTTCAGAGAGCAGAGCGCAAGGCG 1260
DB 1201 GTACACAGATGGAGTGAACATGAAGAGTTCATCTTTCAGAGAGCAGAGCGCAAGGCG 1260
OY 1261 CTGACCAACTGCGGGAACAGCGCCCAAGGAGGAAGAGTTCGGAACACGGACATGCTG 1320
DB 1261 CTGACCAACTGCGGGAACAGCGCCCAAGGAGGAAGAGTTCGGAACACGGACATGCTG 1320
OY 1321 ATGGCGCAGATGATCGCGAGCGGAGCGCCAGCGGAGCAGTGGCGGATGCTGACCGG 1380
DB 1321 ATGGCGCAGATGATCGCGAGCGGAGCGCCAGCGGAGCAGTGGCGGATGCTGACCGG 1380

Oy	901	ATGATCATCATGAGAGATGGCCCTTGAGAGATCCAGACCGGGCAGAGCTCATCAAGGGGGCG	960
Db	901	ATTATATATCATGGAAGATGGCCCTTGAGAGATCCAGACCGGGGAGAGCTCATCAAGGGGGCG	960
Oy	961	CCCGTGTGAGACCAGCAACAAGTTCTCTGTGGTTCCACGCCCCGACACTGAGGGTCTCTTC	1020
Db	961	CCCGTGTGAGACCAGCAACAAGTTCTCTGTGGTTCCACGCCCCGACACTGAGGGTCTCTTC	1020
Oy	1021	TTCATCACCTGACGCTGTCCAGAAATGGGTTTCAGATGGGCACATTTTGTCTGACACTG	1080
Db	1021	TTCATCACCTGACGCTGTCCAGAAATGGGTTTCAGATGGGCACATTTTGTCTGACACTG	1080
Oy	1081	GCCACGCCCGGGCTTGAAGAAATGCTTCCATATGACACATCGGTGAGCATGTAAGGTC	1140
Db	1081	GCCACGCCCGGGCTTGAAGAAATGCTTCCATATGACACATCGGTGAGCATGTAAGGTC	1140
Oy	1141	GTCGTGGGGCTGGCTCTTCAAGTTCTCTGACACTATATCACATTCCCCCTTAGCGGCTC	1200
Db	1141	GTCGTGGGGCTGGCTCTTCAAGTTCTCTGACACTATATCACATTCCCCCTTAGCGGCTC	1200
Oy	1201	GTCACACAGATGGGATGCGAATGAAGAAGTCCATCTTCGACGAGACGGCCAAAGCG	1260
Db	1201	GTCACACAGATGGGATGCGAATGAAGAAGTCCATCTTCGACGAGACGGCCAAAGCG	1260
Oy	1261	CCTACCACTGGCCGGAACAGGGCCAAGGAAGAAGATCCGAGACAGSACATGCTG	1320
Db	1261	CCTACCACTGGCCGGAACAGGGCCAAGGAAGAAGATCCGAGACAGSACATGCTG	1320
Oy	1321	ATGGCGCAGATGATGGCGAGCGGACGCCACGAGCAGCATGTGCGCTAGCGCTG	1380
Db	1321	ATGGCGCAGATGATGGCGAGCGGACGCCACGAGCAGCATGTGCGCTAGCGCTG	1380
Oy	1381	GCTTGTCTCACCGGTGACACCTGCTTCAACAAGGGCATGGGAGGGTCCGACATCCCAAGGC	1440
Db	1381	GCTTGTCTCACCGGTGACACCTGCTTCAACAAGGGCATGGGAGGGTCCGACATCCCAAGGC	1440
Oy	1441	GCGCGCAGCTGCGCCAAAGACCATGAGAGAGCTGAGGACATGTACCCGGTTGTGTGGCG	1500
Db	1441	GCGCGCAGCTGCGCCAAAGACCATGAGAGAGCTGAGGACATGTACCCGGTTGTGTGGCG	1500
Oy	1501	CATCCCGGTGACAGACTTAATCTCGCTGACAGAGCGAGATGGGTCTCTTCGTCGGCACTC	1560
Db	1501	CATCCCGGTGACAGAGCTTAATCTCGCTGACAGAGCGAGATGGGTCTCTTCGTCGGCACTC	1560
Oy	1561	GATGCCGACATCCCAGCGCAGATTTTCTCTCAGCCAGSGATGAGACAAGTTTATGTAT	1620
Db	1561	GATGCCGACATCCCAGCGCAGATTTTCTCTCAGCCAGSGATGAGACAAGTTTCTGTAT	1620
Oy	1621	TGATGTTAGTCCATGTTATGSCCAATATGATGATGTCATGATGTCATATAAGAAATGA	1680
Db	1621	TGATGTTAGTCCATGTTATGSCCAATATGATGATGTCATGATGTCATATAAGAAATGA	1680
Oy	1681	ATTTTTTACTGA 1692	
Db	1681	AATTTTTACTGA 1692	
<hr/>			
RESULT_4			
AAZ30409			
ID	AAZ30409	standard; DNA, 1868 bp.	
XX	AAZ30409;		
XX	21-DEC-1999	(first entry)	
DE	Wheat Mlo fungal resistance gene TrmJOL.		
KM	Consensus, resistance; fungus: pathogen; wheat: cell wall; apposition;		
KM	papilla; contact site; callose; carbohydrate; phenol; transgenic plant		
XX	Mlo; Erysiphe graminis; powdery mildew; ss.		
OS	Triticum sp.		

FH	Key	Location/Qualifiers
FT	CDS	176..1780
FT	/Lag- ^a	
FT	/product=	"fungal resistance protein Mlo1"
XX		
PN	M0947552-A2.	
XX		
PD	23-SEP-1999.	
XX		
PF	17-MAR-1999;	99MO-EP01779.
XX		
PR	17-MAR-1998;	98US-0042763.
XX		
PA	(NOVS) NOVARTIS AG.	
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.	
XX		
P1	Salmerton JM, Welsio LJ, Strawn LJ, Kramer CM;	
XX		
DR	WPI; 1999-571820/48.	
DR	P-PSDB; AAY26966.	
XX		
PT	New proteins useful for generating transgenic plants resistant to	
PT	fungal infection -	
XX		
PS	Claim 2; Page 58-60; 102pp; English.	
XX		
CC	This sequence represents the coding region for the wheat fungal	
CC	resistance gene TrMLO1. The Mlo protein confers resistance to fungal	
CC	pathogens by stimulating the formation of large cell wall appositions,	
CC	designated papillae, at the contact site with the fungal pathogen.	
CC	These papillae mainly contain callose, but also contain carbohydrate,	
CC	phenols and proteases and are used to prevent penetration of the fungal	
CC	hyphae into the plant. The new Mlo sequences are used to generate	
CC	transgenic plants resistant to fungal pathogens, especially Erysiphe	
CC	graminis (powdery mildew).	
XX		
SQ	Sequence 1868 BP: 399 A; 565 C; 521 G; 383 T; 0 other:	
Query Match	94.5%; Score 1616.2; DB 20; Length 1868;	
Best Local Similarity	97.2%; Pred. No. 0;	
Matches 1645; Conservative	0; Mismatches 48; Indels 0; Gaps	
OY	1 ATGGCGGAGACTACGAGTACCCTGGCGGGACGTGCCGAGAACCCCTCTGGGGC 60	
DB	176 ATGGCGGAGCGAGCGAGTACCCCCACGGAGACGCTGCCGGAAGACCGCTCTGGGGC 235	
OY	61 GTGGCGCTGCCTTCGCGCATGATCATCTGTCTCGCTCCTCTGAGACAGCGCTCCAC 120	
DB	236 GTGGCGCTGTCTTCGCGCATGATCATCTGTCTCCTCTCTGTGACAGCGCTCCAT 295	
OY	121 AACCTCGGCATTGGTTCCACAAGCGGCAAGAAGCGCTGGCGGAGGCGCTTGAGAG 180	
DB	296 AACCTCGGCATTGGTTCCACAAGCGGCAAGAAGCGCTGGCGGAGGCGCTTGAGAG 355	
OY	181 ATCAAAGCGAGCTGATGCTGGGGGTTTCATCTCGCTGCTGCTGCCGTAGCCAGAGC 240	
DB	356 ATCAAAGCGAGCTGATGCTGGGGGTTTCATCTCGCTGCTGCTGCCGTAGCCAGAGC 415	
OY	241 CCATATTCGGGATATGATATCTCCGAAAGGCCCCACAGCATATGCGGCGCTGCAAGCT 300	
DB	416 CCATATTCGGGATATGATATCTCCGAAAGGCCCCACAGCATATGCGGCGCTGCAAGCT 475	
OY	301 CCCCGTGTCCGTCGACAGAGCAAGTACAAAATACATACAGCGCCAAAAAAGGCAAGGTG 360	
DB	476 CCCCGTGTCCGTCGACAGAGCAAGTACAAAATACATACAGCGCCAAAAAAGGCAAGGTG 535	
OY	361 TGCGTAATATGTCACAGGCGAGCTTGACCAAGCTCACATATTCATCTTGTGTCTGGCGTC 420	
DB	536 TGCGTAATATGTCACAGGCGAGCTTGACCAAGCTCACATATTCATCTTGTGTCTGGCGTC 595	
OY	421 TTTCATGTCACCTACAGCTCATCATATGCTCTTAAGCGCTCTCAAAATAGGACATGG 480	
DB	596 TTTCATGTCACCTACAGCTCATCATATGCTCTTAAGCGCTCTCAAAATAGGACATGG 655	

Db	1256	GCACGCCCGCGCTTAAAGAAATGCTTCATATGCAATCGGCGCTAGACATCATGAAGATC	1313	
Qy	1141	GTGCTGGGGCTGGCTCTTCAAGTTCTCTGCACTATATACCTTCCCTCTACGGCTC	1200	
Db	1316	GTGCTGGGGCTGGCTCTTCAAGTTCTCTGCACTATATACCTTCCCTCTACGGCTC	1379	
Qy	1201	GTACACACATAGGATCGACATGAGAGAGGTGCATCTTCGACGAGACAGAGGCGCAAGCG	1266	
Db	1376	GTACACACATAGGATCGACATGAGAGAGGTGCATCTTCGACGAGACAGAGGCGCAAGCG	1435	
Qy	1261	CTGACCAACTGGCGGGAACACGCGCCAGAGAGAAAGAGGTCCAGACACGACATGCTG	1320	
Db	1436	CTGACCAACTGGCGGGAACACGCGCCAGAGAGAAAGAGGTCCAGACACGACATGCTG	1499	
Qy	1321	ATGCGCGAGATGATGCGGAGCGAGCGCCACCGAGCGACGTCGCCGATGCTTACCGG	1380	
Db	1496	ATGCGCGAGATGATGCGGAGCGAGCGCCACCGAGCGGCGTCCGCTTACCGGCGG	1559	
Qy	1381	GCATTCTCACCGGTGCACCTGCTTCAAGAGGCGATGGAGCGGTCCGACGATCCCGAGAC	1440	
Db	1556	GGCTCGTCCGCTGCTGCTTCAAGAGGCGATGGAGCGGTCCGACGATCCCGAGAC	1615	
Qy	1441	GGCGCGACCTCGCCCAAGAGACATGAGAGAGCTAGGACATGTACCGGTGTGGTGGCG	1500	
Db	1616	ACCGCAACTGCGCCCAAGAGGCGATGAGAGAGCTAGGACATGTACCGGTGTGGTGGCG	1679	
Qy	1501	CATCCCGTGCACAGACTAAATCTGCTGACAGGCGAGAGTGGTCTTCTGTCGGCACTC	1560	
Db	1676	CATCCCGTGCACAGACTAAATCTGCTGACAGGAGAGAGTGGTCTTCTGTCGGCACTC	1739	
Qy	1561	GATGCCGACATCCCGAGCGCGAGATTTTCTTCACGCGAGGATGAGCAAGTTATGTAT	1620	
Db	1736	GATGCCGACATCCCGAGCGCGAGATTTTCTTCACGCGAGGATGAGCAAGTTATGTAT	1795	
Qy	1621	TGATGTTAGTCCATATGTATGACCAATATGATGTATGATTCGTACATATGAAGATAGA	1680	
Db	1796	TGATGTTAGTCCATATGTATGACCAATATGATGTATGATTCGTACATATGAAGATAGA	1855	
Qy	1681	ATTTTTTACTGAG 1693		
Db	1856	ATTTTTTACTGAG 1868		
RESULT 6				
AA230411				
ID	AA230411	standard; DNA; 1886 BP.		
XX				
XX	AA230411;			
AC				
XX				
DT	21-DEC-1999	(first entry)		
XX				
DE	Wheat Mlo fungal resistance gene TmMlo3.			
XX				
KW	Consensus: resistance; fungus; pathogen; wheat; cell wall; apposition;			
KW	pep11a; contact site; callose; carbohydrate; phenol; transgenic plant			
KW	Mlo; Erysiphe graminis; powdery mildew; ss.			
XX				
OS	Triticum sp.			
XX				
FH	key	Location/Qualifiers		
FT	CDS	198..1802		
FT	/*tag= a			
XX	/product= "fungal fusion protein Mlo3"			
PN	W09947552-A2.			
XX				
PD	23-SEP-1999.			
XX				
FE	17-MAR-1999;	99WO-EP01779.		
XX				
PR	17-MAR-1998;	98US-0042763.		
XX				
ZA	(NOVS) NOVARTIS AG.			

PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.

XX Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;

XX WPI: 1999-571820/48.

DR P-PDB: AAY26968.

XX New proteins useful for generating transgenic plants resistant to
PT fungal infection -

PS Claim 2: Page 68-70; 102pp; English.

XX This sequence represents the coding region for the wheat fungal
CC resistance gene TmL03. The L0 protein confers resistance to fungal
CC pathogens by stimulating the formation of large cell wall appositions,
CC designated papillae, at the contact site with the fungal pathogen.
CC These papillae mainly contain callose, but also contain carbohydrate,
CC phenols and proteins and are used to prevent penetration of the fungal
CC hyphae into the plant. The new L0 sequences are used to generate
CC transgenic plants resistant to fungal pathogens, especially Erysiphe
CC graminis (powdery mildew).

XX Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

Query Match 91.8%; Score 1570.6; DB 20; Length 1886;

Best Local Similarity 95.6%; Pred. No. 0;

Matches 1615; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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OY 1 ATGCGGAGAGACTACGATACCCCGCGGAGAGCTCCGAGAGCGGCTCTGGGCG 60
DB 198 ATGCGAAGAGGAGGAGTACCCCGCGGAGAGCTCCGAGAGCGGCTCTGGGCG 257
OY 61 GTGGCGCTGCTTCCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 258 GTGGCGCTGCTTCCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
OY 121 AAGCTGGCCATTGGTCCACAAAGCGGCAAGAAAGCGGCTGGGAGGCGCTGGAGAG 180
DB 318 AAGCTGGCCATTGGTCCACAAAGCGGCAAGAAAGCGGCTGGGAGGCGCTGGAGAG 377
OY 181 ATCAAGCGGAGCTGATGCTGTGGGCTTCATCTCCCTCTCTCTCTCTCTCTCTCTCT 240
DB 378 ATGAAGCGGAGCTGATGCTGTGGGCTTCATCTCCCTCTCTCTCTCTCTCTCTCTCT 437
OY 241 CCAATCTCGGGATATGATCTCGGAGAGGCGGCGAGATATGCGGCGCTGGAGCGT 300
DB 438 CCAATCTCGGGATATGATCTCCGAGAGGCGGCGAGATATGCGGCGCTGGAGCGT 497
OY 301 CCCCCTGGTTCGCTAAGAGAGATACAAAGACTACTACTGCGCCAAAAGGCGAAGTG 360
DB 498 GAACCGGTTCCGTCAAGAGCAAGTACAGAGACTACTACTGCGCCAAAAGGCGAAGTG 557
OY 361 TCGCTAATGTCCAGCGGAGCTGACACAGCTCACAATTTTATTTTATTTTATTTTATTT 420
DB 558 GCGCTCATGTCCAGCGGAGCGCTGACACAGCTCACAATTTTATTTTATTTTATTTTATTT 617
OY 421 TTCATGTACCTACAGGCTCATCATGCTGTAAAGCGCTCTCAAAATGAGACATGG 480
DB 618 TTCATGTACCTACAGGCTCATCATGCTGTAAAGCGCTCTCAAAATGAGACATGG 677
OY 481 AAGAATGGAGAGAGAGAGCGGCTCTTGGATATACAGTTTGGCAATGATCGAGCGG 540
DB 678 AAGAATGGAGAGAGAGAGCGGCTCTTGGATATACAGTTTGGCAATGATCGAGCGG 737
OY 541 TTCGCTTACGCGACAGAGCTGTGTGAAAGGCGACCTGGGCTCTTCAGACAGCCCG 600
DB 738 TTCGCTTACGCGACAGAGCTGTGTGAAAGGCGACCTGGGCTCTTCAGACAGCCCG 797
OY 601 GGCATCAGATGGGTGGCTTCTTCAGGAGCTTTTAAAGTGGGTGACAAAGTGGAG 660
DB 798 GGCATCAGATGGGTGGCTTCTTCAGGAGCTTTTAAAGTGGGTGACAAAGTGGAG 857
OY 661 TACCTCACCCTGAGGCGAGCTTCATCAAGCGCATTTTGTCCATACAGCAAGTTTCAG 720
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DB 858 TACCTCACCCTTGGAGGCGAGGCTTCATCAAGCGCATTTTGTCCAGAGCAAGTTTCAG 917
OY 721 TTCACAAAGTACATCAAGAGGTCCATGAGAGAGCATTTCAAAGTGTGTTGGCATCAGC 780
DB 918 TTCACAAAGTACATCAAGAGGTCCATGAGAGAGCATTTCAAAGTGTGTTGGCATCAGC 977
OY 781 CTCGCGGTGGGTGGGCGATGCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
DB 978 CTCGCGGTGGGTGGGCGATGCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1037
OY 841 CTCACCTGATTTCTTTCATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
DB 1038 CTCACCTGATTTCTTTCATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1097
OY 901 ATGATCATCATGAGAGATGGCCCTTGAGATCCAGAGACCGGCGAGCTCATCAAGGGGCG 960
DB 1098 ATGATCATCATGAGAGATGGCCCTTGAGATCCAGAGACCGGCGAGCTCATCAAGGGGCG 1157
OY 961 CCGGTGGTGAAGCCAGCAAAAGTTCCTGCTTCCACCGCCGAGCTGGGTCTCTCTCTCT 1020
DB 1158 CCGGTGGTGAAGCCAGCAAAAGTTCCTGCTTCCACCGCCGAGCTGGGTCTCTCTCTCT 1217
OY 1021 TTCATACACCTGAGCGCTGTTCCAGAAATGCTTTCAGATGGACATTTCTGTGACAGTG 1080
DB 1218 TTCATACACCTGAGCGCTGTTCCAGAAATGCTTTCAGATGGACATTTCTGTGACAGTG 1277
OY 1081 GCGACGCGCGGCTTGAAGAAATGCTTCATATGACATGCTTGGAGCATCATGAGAGTTC 1140
DB 1278 GCGACGCGCGGCTTGAAGAAATGCTTCATATGACATGCTTGGAGCATCATGAGAGTTC 1337
OY 1141 GTGCTGGGCGCTGCTTTCAGTTCCTCTGTGACATATATACCTTCCCTCTCTCTCTCT 1200
DB 1338 GTGCTGGGCGCTGCTTTCAGTTCCTGTGACATATATACCTTCCCTCTCTCTCTCTCT 1397
OY 1201 GTGCACAGATGGGATCGAAACATGAAGAGTTCATCTTCAGAGAGAGAGCGGCGCAAG 1260
DB 1398 GTGCACAGATGGGATCGAAACATGAAGAGTTCATCTTCAGAGAGAGAGCGGCGCAAG 1457
OY 1261 CTGACCAACTGGCGGAAACACGCGCAAGAGAGAGAGTCCGAGACACGAGCATCTGTG 1320
DB 1458 CTGACCAACTGGCGGAAACACGCGCAAGAGAGAGAGTCCGAGACACGAGCATCTGTG 1517
OY 1321 ATGGCGCATGATCGGCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380
DB 1518 ATGGCGCATGATCGGCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1577
OY 1381 GCTTGTACCGGTGCACTGCTTTCACAAAGGCGATGGAGGCTCCAGCATCCCAAGAGC 1440
DB 1578 GCTTGTACCGGTGCACTGCTTTCACAAAGGCGATGGAGGCTCCAGCATCCCAAGAGC 1637
OY 1441 GCGCGCATGCGCCAGAGGAGCATGAGAGGCTAGAGGAGCATGTAACCGGTTGTGGTGGC 1500
DB 1638 GCGCGCATGCGCCAGAGGAGCATGAGAGGCTAGAGGAGCATGTAACCGGTTGTGGTGGC 1697
OY 1501 CATCCGCGGAGACAGATCAATCTGTGACAGCGGAGGCTGCTCTCTCTCTCTCTCTCT 1560
DB 1698 CATCCGCGGAGACAGATCAATCTGTGACAGCGGAGGCTGCTCTCTCTCTCTCTCTCT 1757
OY 1561 GATGCGGAGATCCCGAGAGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
DB 1758 GATGCGGAGATCCCGAGAGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1817
OY 1621 TGATTTTATGTCATATGATGAGCAATATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1818 TGATTTTATGTCATATGATGAGCAATATGATGATGATGATGATGATGATGATGATGAT 1877
OY 1681 ATTTTATGAC 1689
DB 1878 ATTTTATGAC 1886
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RESULT 7

AAF24585
ID AAF24585 standard; DNA; 1886 BP.
XX
AC AAF24585:
XX
DI 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of the wheat Mlo protein Trm103.
XX
KW Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
XX powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
OS
XX
XX Triticum sp.
FH Key Location/Qualifiers
FT CDS 198..1802
FT /tag= a
FT /product= "Mlo protein"
XX
PN W0200078799-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000MO-EP05576.
XX
PR 18-JUN-1999; 99US-0336112.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;
PI Vernool J, Levin JZ, Hellefz PB, Patton DA, Que Q;
XX
DR WPI: 2001-112311/12.
DR P-PSDB; AAB31252.
XX
PT Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT producing fungal resistant plants, in particular wheat plant -
XX
PS Claim 2: Page 97-99; 128pp; English.
XX
CC The present sequence encodes a Mlo protein. Mlo proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC Mlo proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC locus are responsible for a plant resistant phenotype. The mechanism
CC of Mlo resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding Mlo proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.
XX
SQ Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other:
Query Match 91.8%; Score 1570.6; DB 22; Length 1886;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1615; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 1 ATGGCGAGACACTACGAGTACCCCGGCGGAGAGCGTCCGAGAGCGGCTGGGCG 60
DB 198 ATGGCAAGAGACGAGGCTACCCCGGCGGAGAGCGTCCGAGAGCGGCTGGGCG 257
QY 61 GTGGCGCTCGTTCGCGGCTGATGATCGTTCGCTCTCGAGAGACGCGCTCCAC 120
DB 258 GTGGCGCTCGTTCGCGGCTGATGATCGTTCGCTCTCGAGAGACGCGCTCCAC 317
QY 121 AAGCTCGGCAATGGTTCCACAAGCGGCAAGAAGCGGCTGGGAGCGCTGAGAAG 180
DB 318 AAGCTCGGCAATGGTTCCACAAGCGGCAAGAAGCGGCTGGGAGGCGCTGAGAAG 377
QY 181 ATCAAGCGAGAGCTGATGCTGGGAGTTTCATCTGCTGCTCGCTCGGCTGAGAGAC 240
DB 378 ATGAAGCGGAGCTGATGCTGGGAGTTTCATCTGCTGCTCGCTCGGCTGAGAGAC 437

OY 241 CCAATCTCCGGGATATGATCTCCAGAAAGCCGAGCATGATCGGAGCCCTGAGCTG 300
DB 438 CCAATCTCCGGGATATGATCTCCAGAAAGCCGAGCATATGCGCCCTGGAAGTG 497
OY 301 CCCCCTGTTCCGTCAAGAGCAAGTACAAAGACTACTACTGCGCCAAAAGGCAAGTG 360
DB 498 GAACCCGGTTCCGTCAAGAGCAAGTACAAAGACTACTACTGCGCCAAAAGGCAAGTG 557
OY 361 TCGCTAATGTCCAGCGGAGCTTCACACAGCTCCACATATTCATCTTGTGCTGCGCTG 420
DB 558 GCGCTATGTCCAGCGGAGCTTCACACAGCTCCACATATTCATCTTGTGCTGCGCTG 617
OY 421 TTCATGTACCTACAGCGTATCATGATGCTTAAGCGCTCTCAAAATGAGACATG 480
DB 618 TTCATGTACCTACAGCGTATCATGATGCTTAAGCGCTCTCAAAATGAGACATG 677
OY 481 AAGAAATGGAGACAGAGACCGCTCCCTTGGAAATACATGTCGCAAAATGATCCTGCGCG 540
DB 678 AAGAAATGGAGACAGAGACCGCTCCCTTGGAAATACATGTCGCAAAATGATCCTGCGCG 737
OY 541 TTCGCTTACGACACAGAGCTGTTCTGAAGCGGACCTGGGCTCTCCAGACCCCG 600
DB 738 TTCGCTTACGACACAGAGCTGTTCTGAAGCGGACCTGGGCTCTCCAGACCCCG 797
OY 601 GGCATGATGGAGTGGTGGCTTCTTCAGGCAATTTTCAGGTCGCTCACAAGGTGAC 660
DB 798 GCGCTGATGGAGTGGTGGCTTCTTCAGGCAATTTTCAGGTCGCTCACAAGGTGAC 857
OY 661 TACCTACCCCTGAGGCGAGGCTTCATCAACGCGCATTTGTCATCAACGCAAGTTGAC 720
DB 858 TACCTACCCCTGAGGCGAGGCTTCATCAACGCGCATTTGTCATCAACGCAAGTTGAC 917
OY 721 TTCACAGATCATCAAGAGTCCATGAGAGAGCTTCAAGTGTGCTGGCATGAC 780
DB 918 TTCACAGATCATCAAGAGTCCATGAGAGAGCTTCAAGTGTGCTGGCATGAC 977
OY 781 CTCGCCGTGTGTGTGGGATCTCAACCTTCTTCTTGTATTTGACGGGATGGCACG 840
DB 978 CTCGCCGTGTGTGTGGGATCTCAACCTTCTTCTTGTATTTGACGGGATGGCACG 1037
OY 841 CTCACATGATTTCTTATCCCTCTCTGATCTCTTGTGTGGAACCAAGCTGAC 900
DB 1038 CTCACATGATTTCTTATCCCTCTCTGATCTCTTGTGTGGAACCAAGCTGAC 1097
OY 901 ATGATCATATGAGATGAGCCCTTGAATCCAGAGACGCGGAGCTATCAAGGGGCG 960
DB 1098 ATGATCATATGAGATGAGCCCTTGAATCCAGAGACGCGGAGCTATCAAGGGGCG 1157
OY 961 CCGGTGTTGAGCCGACAGCAAGTTCTTGTGTTCCACGCGCCGAGCTGGTCTCTTC 1020
DB 1158 CCGGTGTTGAGCCGACAGCAAGTTCTTGTGTTCCACGCGCCGAGCTGGTCTCTTC 1217
OY 1021 TTCATACACCTGACGCTGTTCCAGATGCTTTTCAATGAGCAATTTGTTGAGACGTG 1080
DB 1218 TTCATACACCTGACGCTGTTCCAGATGCTTTTCAATGAGCAATTTGTTGAGACGTG 1277
OY 1081 GCAACGCGCGGCTTAAAGAAATGCTTCATATGACATGATGGCTGAGCATCAAGATG 1140
DB 1278 GCAACGCGCGGCTTAAAGAAATGCTTCATATGACATGATGGCTGAGCATCAAGATG 1337
OY 1141 GTGCTGGGCTGAGCTTCAATGCTCTGAGATATATACCTTCCCTCTACGCGCTC 1200
DB 1338 GTGCTGGGCTGAGCTTCAATGCTCTGAGATATATACCTTCCCTCTACGCGCTC 1397
OY 1201 GTCAACAGATGGATCAAGATCAAGATGATGATGAGAGACAGGACGCAAGGCG 1260
DB 1398 GTCAACAGATGGATCAAGATCAAGATGATGATGAGAGACAGGACGCAAGGCG 1457
OY 1261 CTGACCAATGCGGAGACAGGCGCAAGAGAAAGAAAGTCCGAGACAGGAGCATGCTG 1320
DB 1458 CTGACCAATGCGGAGACAGGCGCAAGAGAAAGAAAGTCCGAGACAGGAGCATGCTG 1517


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Db 1067 CTGGATTCTTTCATCCCTCTGATCTCTCTGTGTGGACCAAGCTGAGATGAT 1126
Oy 906 CATTGATGAGATGGCCCTGGAGATCCAGAGCCGGGAGACGTATCAAGGGGGCCCGT 965
Db 1127 CATCATGAGATGGCCCTGGAGATCCAGAGCCGGGAGACGTATCAAGGGGGCCCGT 1186
Oy 966 GGTGAGCCCGAGAACAAAGTCTCTGTGATCCACGCCCGGAGCTGGTCTCTTCAT 1025
Db 1187 GGTGAGCCCGAGAACAAAGTCTCTGTGATCCACGCCCGGAGCTGGTCTCTTCAT 1246
Oy 1026 ACACGTGAGCTGTTCAGAAATGCGTTTCAGATGGACAAATTCGTCTGACAGTGGCCAC 1085
Db 1247 ACACGTGAGCTGTTCAGAAATGCGTTTCAGATGGACAAATTCGTCTGACAGTGGCCAC 1306
Oy 1086 GCCCGGCTTGAAGAAATGCTTCATATGACATCGGTCTGAGCATCATGAAGTCTGCT 1145
Db 1307 GCCCGGCTTGAAGAAATGCTTCACACAGCATCGGCTGAGCATCATGAAGTGTGCT 1366
Oy 1146 GGGGCTGGCTTTCAGTTCCTCTGAGCTATATCAGCTTCCCGCTCTAGCGGCTGTAC 1205
Db 1367 GGGGCTGGCTTTCAGTTCCTCTGAGCTATATGAGCTTCCCGCTCTAGCGGCTGTAC 1426
Oy 1206 ACAGATGGATGAAACATGAAGAGTCCATCTTCAGACGACAGCGCCAAAGGCGCTGAC 1265
Db 1427 ACAGATGGATGAAACATGAAGAGTCCATCTTCAGACGACAGCTCCAAAGCGCTCAC 1486
Oy 1266 CAACGTGGGAGAACGCGCCAGGAGAAAGATCCGAGACAGGACATGTGATGGC 1325
Db 1487 CAACGTGGGAGAACGCGCCAGGAGAAAGATCCGAGACAGGACATGTGATGGC 1546
Oy 1326 GCAGATGATGGCGAGCGGACGCCAGCGGACGTCGCGATGCTTACCGGCGCTTC 1385
Db 1547 TCAGATGATGGCGAGCGGACGCCAGCGGACGTCGTCGCGGATGCCGCGGCTC 1606
Oy 1386 GTACCGGTCACATGCTTTCACAAAGGCTATGGAGGTCGACGATGCCCGAGCGGCC 1445
Db 1607 ATCACCCTGTCACATGCTTTCACAAAGGCTATGGAGGTCGACGATGCCCGAGCGGCC 1666
Oy 1446 GACCTGGCCCAAGGACCATGAGAGGCTAGGACATGTACCGGCTTGTGTGGCATCC 1505
Db 1667 CACCTGGCCCAAGGACCATGAGAGGCTAGGACATGTACCGGCTTGTGTGGCATCC 1726
Oy 1506 CGTGCACAGACTAAATCCTGTGTGACAGGCGAGTGTCTTCTGTCGGCATCTGATGC 1565
Db 1727 GGTGCACAGACTAAATCCTAACGACAGAGAGAGTGTCCGCTGTGTGGCCCTGCAAGC 1786
Oy 1566 CGACATCCCGCAGCGAGATTTTCTCTACGCAAGGATGAGCAAGTTATGTATGATG 1625
Db 1787 CGACATCCCGCAGCGAGATTTTCTCTACGCAAGGATGAGCAAGTTATGTATGATG 1846
Oy 1626 TTAGT-CCAATGTATAGCCCAACATAGATGTATGATTCGTCAATTAAGAAATGAAATTT 1684
Db 1847 TTAGTCCCAATGTATAGCCCAACATAGATGTATGATGTGTCAATTAAGAAATGAAATTT 1906
Oy 1685 TTTTACTGAGTC 1695
Db 1907 TTTTACTGAGTC 1917

RESULT 9
AAV35022
ID AAV35022 standard; DNA; 1602 BP.
AC AAV35022:
XX
XX
XX 13-OCT-1998 (first entry)
XX
XX Hordeum vulgare cv. Ingrid MLO gene.
XX
XX Barley; MLO; mildew; pathogen; resistance; ss.
XX
XX Hordeum vulgare.
XX
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FH Key Location/Qualifiers
FT CDS 1..1602
FT FT /**tag= a
FT FT /product= MLO protein
PN WO9804586-A2.
PD 05-FEB-1998.
XX
XX 29-JUL-1997; 97MO-GB02046.
PF
XX
XX 07-MAR-1997; 97GB-0004789.
XX 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
XX (INNE-) INNES CENT INNOVATIONS LTD JOHN.
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
XX WPI: 1998-159149/14.
XX P-PSDB: AAM59442.
DR
XX
XX New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
XX Claim 2: Fig 2; 150pp; English.
XX
XX The sequence is that of the MLO gene, wild-type MLO exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of MLO function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.
XX
XX Sequence 1602 BP: 336 A; 488 C; 466 G; 312 T; 0 other;
SQ
Query Match 76.9%; Score 1315.2; DB 19; Length 1602;
Best Local Similarity 89.8%; Pred. No. 1e-296;
Matches 1436; Conservative 0; Mismatches 158; Indels 6; Gaps 2;
Oy 9 GGAATGAGATGATACCCCGGCGGAGGAGGCTGGCGGAGAGCGGCTGCGGCGGTGGCGCT 68
Db 6 GGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 65
Oy 69 GGTCTTGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 128
Db 66 GGTCTTGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 125
Oy 129 CCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
Db 126 CCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 185
Oy 189 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245
Db 186 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245
Oy 246 CTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305
Db 246 CTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305
Oy 306 TGTGCTGCTCAAGAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 365
Db 306 TGTGCTGCTCAAGAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 362
Oy 366 AATGTCAGAGGAGAGTGTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
Db 363 CATGTCAGAGGAGAGTGTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
Oy 426 TGTCACTACAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 485
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Db 423 TGTCACTAGACGCTCATCAACATAGCTCTAAGCCGCTCTCAAAATGAGAAATGAGAAGA 482
Qy 486 ATGGAGAGAGAGACGGCTCTTGGAAATACAGTTCGCAAAATATCTCCGCGTTCCG 545
Db 483 ATGGAGAGAGAGACGGCTCTTGGAAATACAGTTCGCAAAATATCTCCGCGTTCCG 542
Qy 546 CTTCACGACACGAGCTGTCTGTAAGGCGGACCTGGGCGCTCTCCAGACACCCCGGCAT 605
Db 543 GTTCACGACACGAGCTGTCTGTAAGGCGGACCTGGGCGCTCTCCAGACACCCCGGCAT 602
Qy 606 CAGATGGGTGGTGGCTCTTTCAGGCAATTCTTCAGGTGGTCCACCAAGTGGACTACT 665
Db 603 CAGATGGGTGGTGGCTCTTTCAGGCAATTCTTCAGGTGGTCCACCAAGTGGACTACT 662
Qy 666 CACCCCTGAGGCGAGCTTCATCAACGCGCATTTGTGCGATTAACGAAAGTTGCATCTTCA 725
Db 663 GACCTTGAGGCGAGCTTCATCAACGCGCATTTGTGCGAAACGAAAGTTGCATCTTCA 722
Qy 726 CAAGTACATCAAGAGTTCATGAGAGACATTCAAAGTCTGTTGGCATCAGCTCC 785
Db 723 CAAGTACATCAAGAGTTCATGAGAGACATTCAAAGTCTGTTGGCATCAGCTCC 782
Qy 786 GCTGTGTGTGGGAGATCCCTCAACCCCTCTCTGATATATGAGGAGATCGCACGCTCAC 845
Db 783 GCTGTGTGTGGGAGATCCCTCAACCCCTCTCTGATATATGAGGAGATCGCACGCTCAC 842
Qy 846 CTGGATTTCTTTTCATCCCTCTCTCTGATATATGAGGAGATCGCACGCTCAC 905
Db 843 CTGGATTTCTTTTCATCCCTCTCTCTGATATATGAGGAGATCGCACGCTCAC 902
Qy 906 CATCATGAGATGAGCCCTGAGATCCAGAGACGGGCGAGCTCATCAAGGCGGCGCCGT 965
Db 903 CATCATGAGATGAGCCCTGAGATCCAGAGACGGGCGAGCTCATCAAGGCGGCGCCGT 962
Qy 966 GGTGAGGCCAGACAAAGTCTTGTGTTCACAGCCGCCAGTGGTCTCTTCTTCAT 1025
Db 963 GGTGAGGCCAGACAAAGTCTTGTGTTCACAGCCGCCAGTGGTCTCTTCTTCAT 1022
Qy 1026 ACACCTGACGCTTCCAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 1085
Db 1023 ACACCTGACGCTTCCAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 1082
Qy 1086 GCGCGGCTTGAAGAAATGCTTCATGCAATGCGATGCGATGCGATGCGATGCGATGCGAT 1145
Db 1083 GCGCGGCTTGAAGAAATGCTTCATGCAATGCGATGCGATGCGATGCGATGCGATGCGAT 1142
Qy 1146 GGGGCTGCTTTCAGTTCCTCTGACGCTATATCACTTCCCTCTACGCGCTCTCAC 1205
Db 1143 GGGGCTGCTTTCAGTTCCTCTGACGCTATATCACTTCCCTCTACGCGCTCTCAC 1202
Qy 1206 ACAGATGGATGGAACATGAAAGGTTCATCTTCGACGAGAGAGAGAGAGAGAGAGAGAG 1265
Db 1203 ACAGATGGATGGAACATGAAAGGTTCATCTTCACGAGAGAGAGAGAGAGAGAGAGAG 1262
Qy 1266 CAACCTGGCGAAACAGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
Db 1263 CAACCTGGCGAAACAGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1322
Qy 1326 GCAGATGATGCGGCGAGCGAGCGGCGAGCGGCGAGCGGCGAGCGGCGAGCGGCGGCTTC 1385
Db 1323 TCAGATGATGCGGCGAGCGAGCGGCGAGCGGCGAGCGGCGAGCGGCGAGCGGCGGCTTC 1382
Qy 1386 GTACCGGTGACCTGCTTCACAAAGGCGATGAGCGGTTCGACGATCCCAAGAGCGCGCC 1445
Db 1383 ATACCCGCTGACCTGCTTCACAAAGGCGATGAGCGGTTCGACGATCCCAAGAGCGCGCC 1442
Qy 1446 GACCTGCGCAAGAGACATGAGAGAGGCTAGGAGCATGTATCCGCGGTGAGTGGAGCATCT 1505
Db 1443 CACCTGCGCAAGAGACATGAGAGAGGCTAGGAGCATGTATCCGCGGTGAGTGGAGCATCT 1502
Qy 1506 CGTGCAAGACTAAATCTGTGACAGCGGAGAGGTGCTCTCTCTGTCGCGCACTGCATGTC 1565
Db 1503 GTGCGACAGACTAAATCTGTGACAGCGGAGAGGTGCTCTCTCTGTCGCGCACTGCATGTC 1562

Qy 1566 CGACATCCCGACGCGAGATTTTCTCTTACGACGAGATCA 1605
Db 1563 CGACATCCCGACGCGAGATTTTCTCTTACGACGAGATCA 1602

RESULT 10
AAV35030
ID AAV35030 standard; cDNA; 1635 BP.

XX
AC AAV35030;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene homologue.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS Hordeum vulgare.
XX
FH Key Location/Qualifiers
FT CDS 1..1635
FT /tag= a
FT /product= MLO protein homologue

PN W09804586-A2.
XX
PD 05-FEB-1998.
XX
PF 29-JUL-1997; 97NO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
DR WPI: 1998-159149/14.
XX
PT P-PSDB; AAM59445.
XX
PS New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
XX resistance
XX
PS Claim 9; Fig 11; 150bp; English.
XX
CC The sequence is that of a homologue of the MLO gene, wild-type MLO
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of MLO function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
XX encoded polypeptide.
XX
SQ Sequence 1635 BP; 315 A; 496 C; 520 G; 304 T; 0 other;

Query Match 56.0%; Score 959; DB 19; Length 1635;
Best Local Similarity 76.7%; Pred. No. 1.2e-213;
Matches 1265; Conservative 0; Mismatches 270; Indels 114; Gaps 3;

Qy 31 CGGAGGCTGCGGAGAGCGGCTGAGGCGGCTGCTGCTGCGCGGTGATGATC 90
Db 22 CGGAGGCTGCGGAGAGCGGCGGCGGCTGAGGCGGCTGCTGCGCGGTGATGATC 81
Qy 91 GTGTCCTCTCTCTGAGAGAGCGGCTGACAAAGTGGCGCATTTGTTCCACAAAGCGCAC 150
Db 82 GTGTCCTCTCTCTGAGAGAGCGGCTGACAAAGTGGCGCATTTGTTCCACAAAGTGGCGC 141
Qy 151 AAGAACCGCTGCGGAGGCGGCTGAGAGATCAAAACGAGACTGATGCTGCTGAGGCTTC 210

Db 142 AAGAGGCGCTTGGGAGGAGCGCTGGAGAAAGATGAGGAGCTCATGCTGGGCTTC 201
Oy 211 ATCTGCTGCTGCTGCGCTGAGCAGAGACCAATCTCCGGATATGCTCCGAGAG 270
Db 202 ATATCCCTGCTGCTCATCTGACGAGAGATCCCTCCAGATGCGATCCAGAGAG 261
Oy 271 GCCGCGAGCATATGCGGCGCTGAGCGCTGCGCTTCCGCTCAAGAGCAAGTAA 330
Db 262 GCCGCGAGAAAGATGCTCCCTGAGAGCTTACAGCGCGCGCGGCGTGGCAAGGCA 321
Oy 331 GAC----- 333
Db 322 GACAAATCACCAGGAGCTTCTGAGCTCCAGGCGAGAGACCCACCGCGGTTCTG 381
Oy 334 -----TACTACTGCGCCAAAAGGAGCAAGGTGTCGTAATGTCACG 375
Db 382 GCTGCCCCGGCGGAGTGAAGCTGTGCGCAAAACAGGCGAGGTGGCGTATGTCAAG 441
Oy 376 GCGAGCTTGCACAGCTCCACATATTCATCTTGTGCTGCGCTCTTCCATGTCACTAC 435
Db 442 GGAAGCATGCAACCACTGACATATTCCTTGTGCTGCGCTCTTCCAGCTTGTAC 501
Oy 436 AGCGTCATCATATGAGCTTACAGCGCTCAAAATGAGACATGAGAAATGGAGACA 495
Db 502 AGCGTCGTCACATGACCTTAAGCGCTCAAAATGAGCAATGAGAAAGTGGAGTGC 561
Oy 486 GAGACCGCTCTCTGGAATACAGATTCGCAATATCTCTGCGGGTTCGGCTTACGAC 555
Db 562 GAGACCGCTCTGAGATGATCAGTTCGAGATATCCATCATCGGAGTTCACGAC 621
Oy 556 CAGAGCTGCTGTGAAGCGACCTGGGCTCTCCAGCACCCCGGATCAGATGGGTG 615
Db 622 CAGAGCATGTGGTGAAGGCGACCTGGGCTCTCCAGCACCCCGGCTCAGATGGGTG 681
Oy 616 GTGGCTTCTTCAAGAGTTCCTTCAAGTTCGCTCAGCAAGTTCGACTCCTGAGG 675
Db 682 GTGGCTTCTTCAAGAGTTCCTTCAAGTTCGCTCAGCAAGTTCGACTCCTGAGG 741
Oy 676 GCAGCTTCTTCAAGCGGATTTGTGCAATACAGCAAGTTCGACTCCTGAGTATC 735
Db 742 CAGGCTTCTTCAAGCGGATTTGTGCAATACAGCAAGTTCGACTCCTGAGTATC 801
Oy 736 AAGAGTTCATGAGAGAGACATTCAAAGTTCGCTTGGCATTCAGCTCCCGTGGGT 795
Db 802 AAGAGTTCATGAGAGAGACATTCAAAGTTCGCTTGGCATTCAGCTCCCGTGGGT 861
Oy 796 GTGGCATTCCTCACCTCTTCTGATATGATGAGCGGATTCGCGCTCAGCTGATTTCT 855
Db 862 GTGGCATTCCTCACCTCTTCTGATATGATGAGCGGATTCGCGCTCAGCTGATTTCT 921
Oy 856 TTTCATCCCTCTGCTGATCCCTTGTGTGTGAGAACAGTTCGAGATGATCATGAGAG 915
Db 922 GTGGTTCCTCTGATCCCTTGTGTGTGAGAACAGTTCGAGATGATCATGAGAG 981
Oy 916 ATGGCCCTGAGATTCAGAGACCGGCGAGCTCATCAAGGGGGCGCGCTGGTTAGGCC 975
Db 982 ATGGCCCGAGAGATTCATGACCGGAGAGCGTCTCAAGGGGTCTCCCGCTGAGGCC 1041
Oy 976 AGCAACAAGTTCCTTGTGTGTGAGAACAGTTCGAGATGATCATGAGAG 1035
Db 1042 AGCAACAAGTTCCTTGTGTGTGAGAACAGTTCGAGATGATCATGAGAG 1101
Oy 1036 CTGTTCCAGAAATGCGTTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1095
Db 1102 CTGTTCCAGAAATGCGTTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1161
Oy 1096 AAGAAATGCTTCCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1155
Db 1162 AAGAAATGCTTCCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1221
Oy 1156 CTGAGTTCTCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1215

Db 1222 GCCAGATCTTGTGAGCTATACCTTCCGCTCTFAGGCGTCTGTCAGCAGATGGGC 1281
Oy 1216 TCGACATGAGAGAGGCTCATCTTCGACGAGCAGAGCGCCAAAGCGCTGACCACTGGCG 1275
Db 1282 TCACATGAGAGAGAGGCTCATCTTCGACGAGCAGAGCGCCAAAGCGCTGACCACTGGCG 1341
Oy 1276 AACAGCGCCAGAGAGAGAGAGGTCGAGACGAGCATGCTGATGGCGCAGATGATC 1335
Db 1342 AAGATGCGCCAGAGAGAGAGAGGCGCGAGAGCGGCGCATGTGATGGCGAGATGGCG 1401
Oy 1336 GCGAGCGGAGCGCCAGCGCAGGCTGCGCGATGCTTACCGGCGCTTGTACCGGTG 1395
Db 1402 GCGGCGGAGCGCGGAGGCTGCGC-----TGTGCGCGGTG 1437
Oy 1396 CACCTCTTCAAGAGGCTATGAGCAGGCTGAGATCCCGAGAGCGCGCGACCTGCGCA 1455
Db 1438 CACCTCTTCAAGAGGCTATGAGCAGGCTGAGATCCCGAGAGCGCGCGACCTGCGCG 1497
Oy 1456 AGGACCATGAGAGAGGCTGAGGATGATGATCCGCGTGTGAGGCGCATCCCGTGCACAGA 1515
Db 1498 AGGCGCGAGAGAGAGGCGCGGCGC-----GTGACAGATCCGCGCGCGAG 1542
Oy 1516 CTAAATCTGCTGACAGCGGAGGCTGCTCTGCTGCGGCACTGATGCGCATTCGCC 1575
Db 1543 GTACCTCTTGTGAGGCGGAGGCTGCGCTGCTGCGCGCGCTGACAGCTCAGATCCC 1602
Oy 1576 AGCGAGATTTTCTTCTGACGAGGATG 1604
Db 1603 GGTGAGATTTTGTGCTTGCAGCAGCAGC 1631

RESULT 11
AAV35028
ID AAV35028 standard; DNA; 1611 bp.
XX
AC AAV35028;
XX
DT 13-OCT-1998 (first entry)
XX
DE Oryza sativa MLO gene homologue.
XX
KW Rice; MLO; mildew; pathogen; resistance; ss.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT CDS 1..1611
FT /tag= a
FT /product= MLO protein homologue
PN WO9804586-A2.
XX
PD 05-FEB-1998.
XX
FE 29-JUL-1997; 97WO-GB02046.
XX
XX 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Buessches R, Panstruga R, Schulzelefer PMJ;
XX
DR WPI; 1998-159149/14.
XX
PT P-PSDB; AAM59444.
XX
PT New isolated MLO gene of barley - used to develop products for the
XX production of transgenic plants which have increased pathogen
XX resistance
XX
PS Claim 6; Fig 10; 150bp; English.
XX

deletion at this position, resulting in a frameshift"

XX MO200036110-A2.
XX 22-JUN-2000.
XX 17-DEC-1999; 99WO-US30181.
XX 18-DEC-1998; 98US-0112737.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX WPI: 2000-431590/37.
XX P-PSDB: AAB01797.
XX New polynucleotide encoding a Mlo homologue polypeptide, useful for
XX creating transgenic plants with altered levels of disease resistance -
XX
XX Claim 2; Page 52; 79pp; English.
XX
XX The present sequence is a putative coding sequence for a Mlo homologue
XX from wheat. It was identified by searching a root and leaf cDNA library
XX for sequences encoding proteins similar to Mlo from Hordeum vulgare
XX (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe
XX graminis f. sp. hordei upon the plant, and its inactivation leads to the
XX priming of disease resistance even if the pathogen is not present. The
XX gene and protein can be used to create transgenic plants which have
XX increased disease resistance, as well as allowing researchers to find
XX other resistance-conferring genes and proteins.
XX
XX Sequence 678 BP; 143 A; 206 C; 199 G; 130 T; 0 other;

Query Match 38.2%; Score 652.8; DB 21; Length 678;
Best Local Similarity 98.8%; Pred. No. 2e-142; 7; Indels 1; Gaps 1;
Matches 668; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 941 CGAGCGTCATCAAGGGGCGCCCGGTGGTGAAGCCCAACAAGTCTTCTGTTCCACC 1000
DB 4 CGAGCGTCATCAAGGGGCGCCCGGTGGTGAAGCCCAACAAGTCTTCTGTTCCACC 63
OY 1001 GCCCGAGCTGGTCTCTTCTTATACAGTGCAGTGTTCAGATGGCTTTCAGATGG 1060
DB 64 GCCCGAGCTGGTCTCTTCTTATACAGTGCAGTGTTCAGATGGCTTTCAGATGG 123
OY 1061 CACATTTCTGTGAGACAGTGGCCAGCCCGCTTGAAGAAATCTTTCATATGACATCG 1120
DB 124 CACATTTCTGTGAGACAGTGGCCAGCCCGCTTGAAGAAATCTTTCATATGACATCG 183
OY 1121 GTCGTGAGCATCAAGAAAGTGTGCTGGGGCTGGCTTTCAGTTCCTCTGACATATATCA 1180
DB 184 GTCGTGAGCATCAAGAAAGTGTGCTGGGGCTGGCTTTCAGTTCCTCTGACATATATCA 243
OY 1181 CTTTCCCTCTTACGCGCTCTGTACACAGATGGAGTGAACATGAAGAGTCCATCTTCG 1240
DB 244 CTTTCCCTCTTACGCGCTCTGTACACAGATGGAGTGAACATGAAGAGTCCATCTTCG 303
OY 1241 ACGAGCAGACGGCCCAAGGCGCTGACCAACTGGCGGAACAGCGCCCAAGGAGAGAAAGG 1300
DB 304 ACGAGCAGACGGCCCAAGGCGCTGACCAACTGGCGGAACAGCGCCCAAGGAGAGAAAGG 363
OY 1301 TCCGAGACAGGACATGCTGATGGGCGCAGATGATGGCGAGCGAGCCCGACCGAGGCA 1360
DB 364 TCCGAGACAGGACATGCTGATGGGCGCAGATGATGGCGAGCGAGCCCGACCGAGGCA 423
OY 1361 CGTCGCGATGCGCTAGCGGGGCTTGTACACGCTGACAGTCTTTCACAAGGCGATGGAGC 1420
DB 424 CGTCGCGATGCGCTAGCGGGGCTTGTACACGCTGACAGTCTTTCACAAGGCGATGGAGC 483
OY 1421 GGTCCGACGATCCCAAGGCGCGCGAGCTGCGCAAGGACCATGAGAGGCTAGGAGCA 1480
DB 484 GGTCCGACGATCCCAAGGCGCGCGAGCTGCGCAAGGACCATGAGAGGCTAGGAGCA 543

OY 1481 TGTACCCGGTGTGTGATGGCGCATCCGTCGACAGACATTAATCTGCTGACAGCGAGGT 1540
DB 544 TGTACCCGGTGTGTGATGGCGCATCCGTCGACAGACATTAATCTGCTGACAGCGAGGT 603
OY 1541 CGGTCTCTTCTGTCGGCACTCGAGTCCGACATCCCAAGCGCAGATTTTCTTACGCAAG 1600
DB 604 CGGTCTCTTCTGTCGGCACTCGAGTCCGACATCCCAAGCGCAGATTTTCTTACGCAAG 662
OY 1601 GATGAGACAACTTAT 1616
DB 663 GATGAGACAACTTAT 678

RESULT 13
AAA52704
ID AAA52704 standard; cDNA; 563 BP.
AAA52704;
AC
XX
XX 27-OCT-2000 (first entry)

XX Soybean Mlo homologue putative coding sequence #2.
XX
XX Soybean; Mlo homologue; disease resistance; ss.
XX
XX Glycine max.

XX Key Location/Qualifiers
XX CDS 2..562
XX /*tag= a
XX /product= "Mlo homologue"
XX /partial
XX /transl_except= (pos:452..455,aa:xaa)
XX /transl_except= (pos:503..505,aa:xaa)
XX /transl_except= (pos:530..532,aa:xaa)
XX /transl_except= (pos:557..559,aa:xaa)
XX /note= "Xaa-unknown"

XX MO200036110-A2.
XX 22-JUN-2000.
XX 17-DEC-1999; 99WO-US30181.
XX 18-DEC-1998; 98US-0112737.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX WPI: 2000-431590/37.
XX P-PSDB: AAB01794.
XX
XX New polynucleotide encoding a Mlo homologue polypeptide, useful for
XX creating transgenic plants with altered levels of disease resistance -
XX
XX Claim 2; Page 47; 79pp; English.

XX The present sequence is a putative coding sequence for a Mlo homologue
XX from the soybean. It was identified by searching a seed cDNA library
XX for sequences encoding proteins similar to Mlo from Hordeum vulgare
XX (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe
XX graminis f. sp. hordei upon the plant, and its inactivation leads to the
XX priming of disease resistance even if the pathogen is not present. The
XX gene and protein can be used to create transgenic plants which have
XX increased disease resistance, as well as allowing researchers to find
XX other resistance-conferring genes and proteins.

XX Sequence 563 BP; 118 A; 171 C; 165 G; 105 T; 4 other;
XX
XX Query Match 32.5%; Score 555.8; DB 21; Length 563;
XX Best Local Similarity 98.9%; Pred. No. 7.8e-120;

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Db 1 CGTATCAAGGGGGGCGCCCGGTGGTGAACCCAGACACAGTCTTCTGGTTCACCCGCC 60
OY 1005 CGACTGGGTCCTCTTCTTCATACACTGACGCTGTTCAGAAATGCGTTTCAGATGGCACA 1064
Db 61 CGACTGGGTCCTCTTCTTCATACACTGACGCTGTTCAGAAATGCGTTTCAGATGGCACA 120
OY 1065 TTTCGCTGACAGTGGCCAGCCCGGCTTGAAGAAATGCTTCATATGCAATCGGCTCT 1124
Db 121 TTTCGCTGACAGTGGCCAGCCCGGCTTGAAGAAATGCTTCATATGCAATCGGCTCT 180
OY 1125 GAGCATCATGAAGTCTGCTGGGGCTGGGCTTTCAGTTCCTCTGACGCTATATCACCTT 1184
Db 181 GAGCATCATGAAGTCTGCTGGGGCTGGGCTTTCAGTTCCTCTGACGCTATATCACCTT 240
OY 1185 CCCCCTCTACGGGCGCTGACACACAGATGGGATGGAACATGAAGAGGTCATCTTCACGA 1244
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OY 1245 GCAGACGGCCAAAGGCGCTGACCAACTGGCGGAACAGGCCCAAGAGAAGAAGTCCG 1304
Db 301 GCAGACGGCCAAAGGCGCTGACCAACTGGCGGAACAGGCCCAAGAGAAGAAGTCCG 360
OY 1305 AGACAGGACATGCTGATGGGGGAGATGATGGGCGAGCGGACGCCACGACGACGTC 1364
Db 361 AGACAGGACATGCTGATGGGGGAGATGATGGGCGAGCGGACGCCACGACGACGTC 420
OY 1365 GCGGATGCTTACGGCGGCTTCTGTCACGCGTGCACCTGCTTCACAAAGGGCATGGACGCTC 1424
Db 421 GCGGATGCTTACGGCGGCTTCTGTCACGCGTGCACCTGCTTCACAAAGGGCATGGACGCTC 480
OY 1425 CGAGATGCCCGAGAGCGCGGCGACCTGCGCAAGAGACATGGAGGGGTTAGAGCATGTA 1484
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OY 1485 CCGGTTGTGTGGCGCATCCCG 1507
Db 541 CCGGTTGTGTGGCGCANCCG 563

RESULT 14
AAV35025
ID AAV35025 standard; DNA; 2425 BP.
XX
AC AAV35025;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene homologue.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS Hordeum vulgare.
XX
PN M09804586-A2.
XX
PD 05-FEB-1998.
XX
PE 29-JUL-1997; 97MO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
XX
PR 29-JUL-1996; 96GB-0015879.
XX
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
XX
DR WPI; 1998-159149/14.
XX
```

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PT New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Disclosure; Fig 6; 150bp; English.
XX
CC The sequence is that of a homologue of the MLO gene, wild-type MLO
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of MLO function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 2425 BP; 525 A; 692 C; 596 G; 612 T; 0 other;
Query Match 29.6%; Score 505.8; DB 19; Length 2425;
Best Local Similarity 78.6%; Pred. No. 6,2e-108;
Matches 705; Conservative 0; Mismatches 57; Indels 135; Gaps 3;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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3	292	17.1	1713	9	US-09-938-842A-2048	Sequence 2048, Ap
4	223.2	13.0	1725	9	US-09-938-842A-1689	Sequence 1689, Ap
5	210.2	12.3	1581	9	US-09-938-842A-1086	Sequence 1086, Ap
6	205	12.0	1491	9	US-09-938-842A-2268	Sequence 2268, Ap
7	139.4	8.1	1471	10	US-09-770-444-164	Sequence 164, App
8	134.6	7.9	1007	10	US-09-770-444-732	Sequence 226, App
9	121.8	7.1	448	10	US-09-770-444-733	Sequence 733, App
10	105	6.1	386	10	US-09-878-574-1249	Sequence 1249, App
11	66	3.9	455	10	US-09-924-035A-887	Sequence 887, App
12	66	3.9	457	10	US-09-770-444-512	Sequence 512, App
13	56	3.3	279	10	US-09-878-574-13167	Sequence 13167, A
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15	45	2.6	8036	9	US-10-101-388-1	Sequence 1, Appl1
16	44.6	2.6	759	10	US-09-887-576-810	Sequence 810, Appl
17	44.4	2.6	2285	10	US-09-878-554A-25	Sequence 25, Appl
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25	44	2.6	2298	10	US-09-476-242-24	Sequence 24, Appl1
26	44	2.6	2529	10	US-09-476-242-14	Sequence 14, Appl1
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41	40.6	2.4	492	10	US-09-867-550-613	Sequence 613, App
42	40	2.3	583	10	US-09-864-761-20772	Sequence 20772, A
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44	40	2.3	1959	10	US-09-864-761-4012	Sequence 4012, Ap
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ALIGNMENTS

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RESULT 1
US-09-938-842A-1347
: Sequence 1347: Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: FILE REFERENCE: SCRIPI300-3
: CURRENT APPLICATION NUMBER: US/09/938, 842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227, 866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1347
: LENGTH: 1710
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-1347

Query Match      21.4%: Score 365.6: DB 9: Length 1710:
Best Local Similarity 56.8%: Pred. No. 9.5e-84:
Matches 730: Conservative 0: Mismatches 529: Indels 27: Gaps 2:

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RESULT 3
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; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2048
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2048

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Best Local Similarity 56.6% Pred. No. 5.8e-65;
Matches 594; Conservative 0; Mismatches 435; Indels 21; Gaps 2;

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Oy 1289 AGAAGAGAGGTCGGAAGACGAGACATGCTGTATGGCCGATGATGAGCGACGCAAGC 1348
Db 1349 AACAGAGCAAAAGTATGAGCAAGTCTTAACACACCTCTACTCGAGCGCTCTACTACGC 1408
Oy 1349 CCAGCCGAGCAGTCCGCGATGCTTACGCC 1378
Db 1409 CACACATGTCATGTCACGCGTGCATCTCC 1438

RESULT 4
US-09-938-842A-1689
; Sequence 1689, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

```
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1689
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1689
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Query Match      13.0%; Score 223.2; DB 9; Length 1725;
Best Local Similarity 51.2%; Pred. No. 2,1e-47;
Matches 705; Conservative 0; Mismatches 548; Indels 123; Gaps 3;
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QY 1 ATGCGGAGAGCTACGAGTACCCCGCGGACGCTCCGAGACGCCGCTCGGCG 60
DB 85 ACGCGAGAGATGAGAGAAAGTGTACATTAACAGCTTAATCAAACTCGAGCTGGCGT 144
QY 61 GTGGCGCTGCTCTGCGCGTATGATCATGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 145 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
QY 121 AAGCTCGGCAATGGTTCACACAGCGGACACAGACGCGCTGGGAGGCGCTGAGAG 180
DB 205 AAGGTGGAAGGTTCTATGGATCGGACACAGACAGCTCTCTGCTGCTGCTGCTGCTG 264
QY 181 ATCAAGCGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 265 ATCAAGCGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 324
QY 241 CCAATCTCCGAGATATGATCTCCGAGAGGCGGACGATCATGCTGCGCCCTGAGCCTG 300
DB 325 TACATTTTGATATTTGATCCCTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
QY 301 CCCCCTGTTCCGTCAGACAGTACAAAG----- 331
DB 385 CTTAAGCTGAAAAAGAGAGATGATGACAAATGGTGAAGATGACAGAGACACTTGTGCTTT 444
QY 332 -----ACTACTGCGCCCAAAAAGGCAAG 357
DB 445 GAGCAGATTTTATATCTGAGGTGAGCATCTCCACTAATTCAGAGAGAGGGTTAT 504
QY 358 GTGTGCTATATGTCACAGGCGAGCTTGACACAGCTCCACATATTCATCTTGTGCTGCGC 417
DB 505 GTAGAGCTTATCTGCGGAGGAGGACCTCCATAGTTGACATCTTATATCTTCTTGAACC 564
QY 418 GTCTTCATGTCACCTACAGCGGTCATCATAGCTCTAAGCCCTCTCAAAATGAGGACA 477
DB 565 ATTTTCACGTTCTTTACAGCTCTTAACTATGATGCTGGAAGTTGAAGATTCGCGGA 624
QY 478 TGGAGAAATGGAGACAGAGACCGCTCTTGAATTCAGATTCGCAAAATGATTCCTGGC 537
DB 625 TGGAGCAATGGAGAAATGAGACATCCCATATTTAGCATTTTCAAGACACTTCC 684
QY 538 CGGTTCGCTTCACGACACAGAGCTGCTGGAAGCGGACCTGGCCCTCT---CCAGC 594
DB 685 AGATTCAGGCTTACATGAAATCTTTTGTGAGAGGCGACACCAATCTTGTGAGCCCGG 744
QY 595 ACCCCGCGCATCAGATGGGTGTGCGCTTCTTACAGGACTCTTCAAGTGGGTGACCAAG 654
DB 745 ATTCATCTCTTTCTATGTTGATGCTTTTTCAGACAGTTTTCATATCCGTTGGGAGA 804
QY 655 GTGAGCTACCTACCGCTGAGGCGAGCTTCAACAGCGCATTTGTGCTAATACAGCAAG 714
DB 805 ACTGACTATTTGACATGAGAAATGTTTCACTGCTGTTCTATTAGCTCCAGGAAGCTCAA 864
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QY 715 TTGCACTTCCACAAATACATCAAGAGTTCATGAGAGACACTTCAAAAGTCTGCTGGC 774
DB 865 TTTAACCTTCAAAAATACATTAATAAGATCGTTGAGGATGATTTTCAAGGTAGCTGTGA 924
QY 775 ATCAGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 834
DB 925 GTACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
QY 835 GGCAGGCTACCTGAGATTTTTCATCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
DB 982 -----ACAAAG 987
QY 895 CTGAGATGATCATCATGAGATGAGCCCTGAGATCCAGAGCCGCGAGCGCTGCTCAAG 954
DB 988 CTTCAAGGATATGACAGAGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
QY 955 GGGGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
DB 1048 GGAATGCGCGCTGTGACAAAGGACATGATGATTTGCTGCTGCTGCTGCTGCTGCTGCT 1107
QY 1015 CTCTCTTCAATACCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
DB 1108 CTTCATCTCATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
QY 1075 ACATGGCCACCGCCGCTTGAAGAAATGCTTCCATATGCAATGCGTGTGACATCATG 1134
DB 1168 ATATGATATCTCTTGTGATCAATTTCTGCTACCATCTTAATTTCAAGATTCGACTGTA 1227
QY 1135 AAGTGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
DB 1228 AAGATGAGATGCTTTAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287
QY 1195 GCGCTGCTACAGAGATGGATGCAATGAAAGGCTCATCTGCTGCTGCTGCTGCTGCTG 1254
DB 1288 GCACTGCTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1347
QY 1255 AAGCGCTGACCACTGGCGGAACAGCGGCAAGGAGAGAGAGCTGCGAGAC 1310
DB 1348 AAGCACTCAAGAAATGAGAAATGCGAGTGAAGAAAGAGTGTGAAGCCAC 1403
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RESULT 5
US-09-938-842A-1086
; Sequence 1086, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Man, Yung
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1086
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1086
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Query Match      12.3%; Score 210.2; DB 9; Length 1581;
Best Local Similarity 53.4%; Pred. No. 4.1e-44;
Matches 493; Conservative 0; Mismatches 418; Indels 12; Gaps 2;
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QY 337 TACTGCGCCAAAAGGCAAGGTGCTGCTATGCTCAGCGGAGCTTGCACACGCTCCAC 396
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||||| ||||||| ||| ||| ||| ||||||| |||
Db 421 TACTGAGCAAAAGGCTAAAGTACATTCCTTCCTTGAGGACATTCGACCATCTACAT 480
Oy 397 ATATTCATCTGCTGCTGCGCTCTCCATGTCACCTACAGGCTCATCATATGCTCTA 456
Db 481 ATTTTCATCTGCTGCTGCGCTCATATCCCATGTCATCTGCTGCTTACCGTATTTT 540
Oy 457 AGCCGTCTCAAAATGAGGACGAAATGGAGACAGAGACGCGCTCCCTTGAATAC 516
Db 541 GGAAAGCAAAAGATTCACCAATGGAAAGATGGAGATTCATCGCAAGATGAGAGATT 600
Oy 517 CAGTTGCAAAATGATCTGCGCGCTCCGCTTACAGC-----ACAGAGCTCGTTC 567
Db 601 GACCCCGAAACAGCTCTCAGGAAAGAGGCTCAGTATGATACACAAACCATCTTTATT 660
Oy 568 GTGAAGCGGACCTGGGCGCTCTCCAGCACCCCGGCA---TCAGATGGTGGTGGCTTC 624
Db 661 AAAGAGCATTTTCTTGATTTGGCAAAAGATTCAGTCACTCGATGGAGAGCGAATCCCTT 720
Oy 625 TTTCAGCAGTTCTTCAAGTCTGCTACACAGGTGACTACCTCACCTGAGGGCAGCTTC 684
Db 721 CTCAAGCAATTCATGATTCCTGTCAGAAATCAGATTAAGTTCAGTCTTGCTTC 780
Oy 685 ATCAAGCGCATTTGTGCATATGACAGAGTTCGACTTCACAAAGTACATCAAGAGTCC 744
Db 781 ATATGACACATTTGTAAGGAAACCCCAAGCTTAATTCCAAAGATATGATGCGGCT 840
Oy 745 ATGAGAGACATTCAAAGTCTGCTTGATGCTACAGCTCCCGCTGCTGCTGCTGCTG 804
Db 841 CTAGAGGATATTTCAACAAAGTCTGATGATGATGATGATGATGATGATGATGATG 900
Oy 805 CTCACCCCTCTCTGATATGATGACGGGATCGGACGCTCAGCTGATTCCTTTCATTCCT 864
Db 901 ATCTTTTGTGCTAAATGTAAGATGACGATGACACATATTTCTGATACATTTATTC 960
Oy 865 CTCGTCATCCTCTGCTGCTGATGACCAAGCTGGAGATGATGATGATGATGATGATG 924
Db 961 TTTGCTTGTCTTCTGCTGCTGATGACCAAGTGGAGCATGATGATGATGATGATGAT 1020
Oy 925 GAGATCCAGAGCGGGGAGGCTCATCAAGGGGCGCGCTGCTGATGAGCCAGCAACAG 984
Db 1021 GAAGTTCAGAGAAACATGATGACCATGAGAGAGACTGATGAGAAACCTTCACATAG 1080
Oy 985 TTTCTGCTGCTCCACGCGCGCGCTGAGGCTCTTCTTCAACCTGAGCGCTTCCAG 1044
Db 1081 CATTTCTGCTTACAGAAACCTCAAAATGTTCTTCTTCACTTTCATTTTATCCTTCCAG 1140
Oy 1045 AATGCTTTAGATGACATTTCTGCTGACAGTGGCCAGCGCGCTTGAAGAAATGC 1104
Db 1141 AATGCTTTAGATGACATTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
Oy 1105 TTCCATATGACATCGGCTGAGCATCATGAAAGTCTGCTGAGGCTGCTCTTCAAGTTC 1164
Db 1201 ATTATGGACAGGTGAGATATCATTTGTTCCAAAGATTTGTTATCGGGGCTTTCATTCAGTG 1260
Oy 1165 CTCTGACGCTATATCATCTTCCCTTACGCGCTCTGACACAGATGGATGCAATG 1224
Db 1261 CTCTGACGCTATATCATCTTCCCTTTCATCGCCATCTTCCACAGATGGAGATGCTTC 1320
Oy 1225 AAGAGTCCATCTTCAGCAGCA 1247
Db 1321 AAGAAAGCTATATTCAGAGGAA 1343

;; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN
;; TITLE OF INVENTION: SAME, AND METHODS OF USE
;; FILE REFERENCE: SCRIPI300-3
;; CURRENT APPLICATION NUMBER: US 60/938,842A
;; CURRENT FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/727,866
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/764,647
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/700,111
;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 2268
;; LENGTH: 1491
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2268
Query Match 12.0%; Score 205; DB 9; Length 1491;
Best Local Similarity 49.3%; Pred. No. 8.5e+43;
Matches 657; Conservative 0; Mismatches 610; Indels 66; Gaps 2;
Oy 33 GACGCTGCCGAGAGCGCGCTCTGAGCGGTGGCGCTCTTCCGCTCATGATCATCGT 92
Db 18 GACCTTAAGATGATACACCACTGGGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCT 77
Oy 93 GTCGCTCTCTGAGCAGCGGCTCCACAGCTCGGCTATGTTCCACAAAGCGGACAA 152
Db 78 CTCTTTTGGCGCTGAGCGCTCTCATTCAGCTGCGGAAAGCATTAAGAACAGTCA 137
Oy 153 GAAGCGCTGCGGAGCGGCTGGAAGATCAAAAGCGGATGATGCTGCTGGGTTCAT 212
Db 138 GAAGCAGCTTTTGGGGGATTAACAAAGATCAAAAGAGATGATGATGATGATGAT 197
Oy 213 CTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 272
Db 198 ATGCTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
Oy 273 CGCAGCATCATCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
Db 258 AAGTGAAGATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
Oy 333 CT----- 334
Db 318 CTCACATTCAGGTTACGCTTACCGGCGCTCATCTCTGCGCGGAGATGCGCGCGG 377
Oy 335 --ACTACTGCGCAAAAGGCAAGGTGGCTAATGCTCCAGCGGACGCTTGCACGCT 392
Db 378 TGACTACTGCTCTCTAAGGAAAGATGACAAATATGATATGATATGATATGATATG 437
Oy 393 CCACATATTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
Db 438 TCATATATTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 497
Oy 453 TCTAAGCGCTCTCAAAATGAGAGCATGGAAGAAAGGAGAGAGAGAGAGAGAGAGAG 512
Db 498 TTTTGTGACATGAAAGATTAAGCAATGGAAGAAAGGAGAGAGAGAGAGAGAGAGAG 557
Oy 513 ATACAGTTCGCAAAATGATCTGCGCGGCTTCCCTTACGCAACAGAGCTGTTCTG 572
Db 558 CTTCGACAGACAGCAAAAGATTAAGAAATTCACACAGCTTCAAGAACAGAAATTCAG 617
Oy 573 GCGGCACTGGGGCTCTCCAGAGACCGCG-----GCATCAGATGGGTGGCTCTCT 626
Db 618 GTCAAGATTTCTTGGGGGTGGAAGAGCTGATGCTCTCTTGGGATGGGATGCAATG 677
Oy 627 CAGCGACTTCTTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686
Db 678 GAACAGCTTTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 737
Oy 687 CAAGCGCATTTGCTCATACAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 746
Db 738 CAGCATCATTTGCAAGAGCAACCAAAATTCATATTTCAATGATTAATGATGCTGCT 797

RESULT 6
US-09-938-842A-2268
; Sequence 2268, Application US/0993842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

Query Match	8.18;	Score 139.4;	DB 10;	Length 471;
Best Local Similarity	58.88;	Pred. No. 2.7e-26;		
Matches 277;	Conservative	0;	Mismatches 185;	Indels 9; Gaps 2.
<p>NUMBER OF SEQ. ID NOS: 999 SOFTWARE: FastSeq for Windows Version 4.0 SEQ ID NO 164 LENGTH: 471 TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE: NAME/KEY: misc-feature LOCATION: (1)...(471) OTHER INFORMATION: n = A,T,C or G US-09-770-444-164</p>				
Query	469	ATGAGACATGGCAAMAATGGAGACAGACAGACCGCCCTTGGAAATACAGTTGGCAAA	528	
Db	1	ATAGAGACCTGGGAATCGTGGGAGAGAGACAAGAACAAATAGATGATCATGATTCACAC	60	
QY	529	GATCCGCGCCGGTCCGCTTCAGCAGCACAGACGTCGTTCGTAAGAGCGGACCTGGGCGTC	588	
Db	61	GATCCGAGAGGTTTACGTTTGGCAGAGGACACATCTTTTGGAGAAAGACATCTCAATTTTC	120	
QY	589	TCCAGCACCCCGGCATCA--GATGGTGGTGGGCTTCCTTCAGGAGTTCTTAGGTGC	645	
Db	121	TGGAGACACAGACAGTGCACATATGATTTGTTTGTATAGAAAGTTCTTTGGATCT	180	
QY	646	GTCACCAAGTGGACTACCTACCTCGAGGCGAGGCTTCATCAACGCGATTTGTCG--	703	
Db	181	GTCACCAAGTTGATTACTTAGCAGCTAAGACATGGTTTTCATCATGGCGATTTTGCTCC	240	
QY	704	----AAACAGCAAGTTCGACTTCACAAATCATCAAGAGTCCATGGAGAGCACTTC	759	
Db	241	GGTACAGATCAAGATTCGATTTTCGCAAGTATATTCAGAGATCATTTGAAAGAACTTC	300	
QY	760	AAAGTCGTGGGCATCAGCCTCCGCGTGTGGTGGCGATCCATCCCTTCCTT	819	
Db	301	AAACCGTGTGTAATACATCGCGGTATCTGGTTNNNNCTGTGCTATCTCTTGAC	360	
QY	820	GATATGACGGGATCGGACGCTCACACGATGATTTCTTCACTCCCTCGTATCCCTCTG	879	
Db	361	AATTCATATGATTAATACGTTCTTACCTCTGTTACCATTCATTCACACTAGTGTATTTCTA	420	
QY	880	TGCTGTTGACCAAGCTGGAGATGATCATCATGAGATGGCCCTCGAGATC	930	
Db	421	ATAGTTGACAAAGCTTGAAATCAATAAACAATAATTTGGTCTTAAGATC	471	
<p>RESULT 8 US-09-770-445-226 Sequence 226, Application US/09770445 Patent No. US20020023281A1 GENERAL INFORMATION: APPLICANT: Goriach, Jörn APPLICANT: An, Yong-Qiang APPLICANT: Hamilton, Carol M. APPLICANT: Price, Jennifer L. APPLICANT: Raines, Tracy M. APPLICANT: Yu, Yang APPLICANT: Rameaka, Joshua G. APPLICANT: Page, Amy APPLICANT: Matthew, Abraham V. APPLICANT: Ledford, Brooke L. APPLICANT: Woessner, Jeffrey P. APPLICANT: Haas, William David APPLICANT: Garcia, Carlos A. APPLICANT: Kricker, Majja APPLICANT: Slader, Ted APPLICANT: Davis, Keith R. APPLICANT: Allen, Keith APPLICANT: Hoffman, Neil APPLICANT: Hurbane, Patrick</p>				

;; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
;; FILE OF INVENTION: thaliana
;; FILE REFERENCE: 202305 (PARA-012PRV)
;; CURRENT APPLICATION NUMBER: US/09/770,445
;; CURRENT FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: US 60/178,472
;; PRIOR FILING DATE: 2000-01-27
;; NUMBER OF SEQ ID NOS: 999
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 226
;; LENGTH: 1007
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)..(1007)
;; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-226

Query Match 7.9%; Score 134.6; DB 10; Length 1007;
Best Local Similarity 53.7%; Pred. No. 6,5e-25;
Matches 278; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

Qy 730 TACATCAAGAGTCATGAGAGACATTTAAAGTCGTTGGATCGACCTCCCGCTG 789
Db 1 TATATGATGGCGCTGAGAGATGATTTCAACAGTTGTTGATTTGATTT 60
Qy 790 TGTGTGTGGCGATCTCACCTCTCTTGATATGACGGGATCGGACCTGCTG 849
Db 61 TGGATCTTGTGCTCATCTTCTTGTGCTAAATGTTAAACGATGACACATATTTGG 120
Qy 850 ATTCTTTTCAATCCCTGCTCATCTCTTGTGTTGTTGAACCAAGCTGGAGATGATC 909
Db 121 ATACATTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 180
Qy 910 ATGAGATGGCCCTGAGATCCAGACCGGCGAGCTCATCAAGGGGCGCCGCTG 969
Db 181 GCACAGTTAGCTCATGATGACAGAAACATGTACCTTAAAGAACTTATGCTG 240
Qy 970 GAGCCGACAAAGATCTTGTGTTCCACCGCCGACGCTGCTCTTCTTCTTAC 1029
Db 241 AAACCTCAAGATGAGATTTCTGTTGACAAACCTCAATTTCTTCTTCTTCTT 300
Qy 1030 CTGACGCTGTTCCAGAAATGCTTGAATGACATGTTGCTGTCGACATGCGCC 1089
Db 301 TTTATCTTCTTCCAGAAATGCTTGAATGACATGCTTCTTCTTCTTCTTCTT 360
Qy 1090 GCTTGAAGAAATGCTTCCATATGACATCGTCTGACATCAAGGCTGCTG 1149
Db 361 GCTTCACTGCTGCTTATATGAGACAGTGAATATGTTTCAAGATTTGTTATCG 420
Qy 1150 CTGGCTCTGATGCTCTGACGATATATCACTTCCCTTACGCGCTGCTACAG 1209
Db 421 GTCTTCATTCAGTCTTCTTCAAGTTCACATGCTTCTTCTTCTTCTTCTTCT 480
Qy 1210 ATGGATCGAAATGAGAGGTCATCTTTCAGACAGA 1247
Db 481 ATGGGAAGTACTTCAAGAAAGTATATTCNAGAGAA 518

RESULT 9
US-09-770-444-733/C
; Sequence 733; Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy

;; APPLICANT: Matthew, Abraham V.
;; APPLICANT: Ledford, Brooke L.
;; APPLICANT: Woessner, Jeffrey P.
;; APPLICANT: Haas, William David
;; APPLICANT: Garcia, Carlos A.
;; APPLICANT: Kicker, Maja
;; APPLICANT: Slader, Ted
;; APPLICANT: Davis, Keith R.
;; APPLICANT: Allen, Keith
;; APPLICANT: Hoffman, Neil
;; APPLICANT: Huban, Patrick
;; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
;; FILE OF INVENTION: thaliana
;; FILE REFERENCE: 2027 (PARA-016PRV)
;; CURRENT APPLICATION NUMBER: US/09/770,444
;; CURRENT FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/178,502
;; PRIOR FILING DATE: 2000-01-27
;; NUMBER OF SEQ ID NOS: 999
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 733
;; LENGTH: 448
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-770-444-733

Query Match 7.1%; Score 121.8; DB 10; Length 448;
Best Local Similarity 58.8%; Pred. No. 8e-22;
Matches 210; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

Qy 954 GGGGGGCGCCGTGTTGAGCCAGACAAAGTTCTTGTGTTCCACCGCCGACCTGG 1013
Db 448 GGTGCGGCGCGAGTACAGCAAGCATGATTTCTGCGCTGCTCCATTTGAT 389
Qy 1014 CCTCTCTTCAATACCGTACGCTGTTCCAGATGCTTCCAGATGACATTTCTG 1073
Db 388 TCTCATCTCATGATTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 329
Qy 1074 GACAGTGGCCAGCGCGCTTGAAGAAATCTTCCATATGACATGCTGACATCAT 1133
Db 328 GATATGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 269
Qy 1134 GAGGTGCTGTTGGGCTGCTCTTCAATGCTTCTGACATATCACTTCCCTCT 1193
Db 268 AAAAGTAGGATTTCTTGAAGATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 209
Qy 1194 CGCGCTGCTCAACAGATGAGATGAAATGAAAGGTCATCTTCCAGAGAGCG 1253
Db 208 CGCATCTGTAAGTCTGATGTTCTGATGAAATGATGATTTCTGATGAAAGGTC 149
Qy 1254 CAAGGCTGACCACTGCGGAACAGCGCCAAAGAGAAAGATTCGAGACAC 1310
Db 148 AAAAGACTCAAGAAATGAGATGAGATGAGAAAGAGATGAGAAAGGTCGAAAG 92

RESULT 10
US-09-878-574-1249
; Sequence 1249; Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;; FILE REFERENCE: 38-21(13401)B
;; CURRENT APPLICATION NUMBER: US/09/878,574
;; CURRENT FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 09/333,535
;; PRIOR FILING DATE: 1999-06-14
;; NUMBER OF SEQ ID NOS: 15775
;; SEQ ID NO 1249
;; LENGTH: 396

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; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-040-Q1-B1-A8
US-09-878-574-1249
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Query Match
Best Local Similarity 57.5%; Score 105; DB 10; Length 396;
Matches 211; Conservative 0; Mismatches 150; Indels 6; Gaps 1;
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OY 938 GGGGAGGCGTCATCAAGGGGGGCGCGTGTGAGCCAGCAACAAGTCTTCTGGTCC 997
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DB 1 GGGGGAGAGTGGTCAAGGGTGCACCTTTGGTGAAGCAAGATATATGTTGGTCA 60
OY 998 ACCGCCCCGACTGGGCTCTCTTCTTCAATACAGCTGAGCGTGTCCAGATCGTTTCA 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 ATCGACCCCGCTCAATCCCTTTTGAATCATCTGTCTCTTTCAGATTCATTCAC 120
OY 1058 TGGACATTTTCTGTGAGACAGTGGCCAGCGCGCTTGAAGAA-----TGCCTCCATA 1111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 TAGCGTTTTTCTGTGAGACACATATGACATGGGTTCATAAATAAATCTGTGTTCCACA 180
OY 1112 TGCACATCGGTCTGAGCATATGAAGGTCTGCTGGGCTGCTCTTCAATTCCTCTGCA 1171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 AAACCTACTGCAGATATTTGTCAATAGACTACATATGGGGTCTCACACAAGTCTATGCA 240
OY 1172 GCTATATCACCTTCCCGCTAGCGGCTGCTACACAGATGGAGTCAACATGGAAGAGT 1231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 GTTATGTGACTTGGCTCTTATAGCTCTTATGCTACCCAGATGGGTCTTCACTGAACCTTA 300
OY 1332 CCATCTTCAGACAGACAGCGCCAGGCGCTGACCAACTGGCGGAACAGCGCAAGGAGA 1291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 CTATTTTCAATGAATAATGTGTGACGTACCTGAGAACTGGCATCACACTGCTTAAAGC 360
OY 1292 AGAAGAA 1298
    ||| |||
DB 361 ACATCAA 367
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RESULT 11
US-09-924-035A-887/C
; Sequence 887, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo, Jm
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 887
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-887
```

```
Query Match
Best Local Similarity 69.2%; Score 66; DB 10; Length 455;
Matches 90; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
```

```
OY 1166 TCTGAGCTATATACCTTCCCTCTAGCGGCTGTACACAGATGGATCGAATCA 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 455 TATGAGCTATACATCTCTCCATGTGAGCCCTGTACTACATAGATGGTTCACATCA 396
OY 1226 AGAGTCCATCTTGCAGACAGACAGCGCCAGCGCTGACCAACTGGCGGAGACAGCGCA 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
DB 395 AGAAGACGCTTTGATGACCAANTGGCAAGGCAATTGAGAGTGGCACAAAGACATCA 336
OY 1286 AGGAGAGAA 1295
    ||| ||| |||
DB 335 AATTGAAGAA 326
```

```
RESULT 12
US-09-770-444-512/C
; Sequence 512, Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jom
; APPLICANT: An, Yong-Oiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kicker, Maya
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 512
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(457)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-512
```

```
Query Match
Best Local Similarity 69.2%; Score 66; DB 10; Length 457;
Matches 90; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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```
OY 1166 TCTGAGCTATATACCTTCCCTCTAGCGGCTGTACACAGATGGATCGAATCA 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 457 TATGAGCTATACATCTCTCCATGTGAGCCCTGTACTACATAGATGGTTCACATGA 398
OY 1226 AGAGTCCATCTTGCAGACAGACAGCGCCAGCGCTGACCAACTGGCGGAGACAGCGCA 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 397 AGAAGCAGTGTGATGAGCAAAATGGCAAGGCAATTGAAGAAGTGGCACAAAGACATCA 338
```

```
OY 1286 AGGAGAGAA 1295
    ||| ||| |||
DB 337 AATTGAAGAA 328
```

```
RESULT 13
US-09-878-574-13167
; Sequence 13167, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
```



```
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(13401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 13167
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701066723H1
US-09-878-574-13167
```

```
Query Match          3.3%  Score 56; DB 10; Length 279;
Best Local Similarity 52.9%; Pred. No. 3.9e-05;
Matches 144; Conservative 0; Mismatches 125; Indels 3; Gaps 1;
```

```
OY 622 TTCTTACGCGAGTTCTTCAGTGGTCCACCAAGGTGAGTACCTCACCCTGAGGGCAGGC 681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 TTCCGCGCCCAATTTTGGAGTTCATCCACAGAGCTGATTACATGCGCTTACAGGC 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 682 TTTCATCAAGCGGCAATTTGCGCATACAGCAAGTGGAGCTTCCACAAGTACATCAAGG 741
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 TTCTATTA---CTATCATAGGCTTTCCCAACATACAGCACTTCCACACTATATGCTTCA 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 742 TTCATGAGAGAGCACTTCAAACTGCTGTCGATCCCTCCCGCTGTGTGTGGCG 801
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 AGCATGAGATAGGAATTTGTCACATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 802 ATCTCACCCCTTCTCTGATATGACGAGATCGACGCTCAGCTGATTTCTTATC 861
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 ATCTGCTGATTTTCTTAATTTTCAGGAGCAACTTTACTTCTGCTGCTTCTTCTT 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 862 CCTCTGCTATCTCTTGTGTGTGAACCA 893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 CCAGCAATTTTGAATCCTTATTCATTTGCTACTAA 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 14
US-10-101-388-2
; Sequence 2, Application US/10101388
; Patent No. US20020162142A1
; GENERAL INFORMATION:
; APPLICANT: Johal, Gurmukh S
; APPLICANT: Multani, Dilbag S
; TITLE OF INVENTION: GENES AND METHODS FOR MANIPULATION OF GROWTH
; FILE REFERENCE: 5718-81 (035718/205794)
; CURRENT APPLICATION NUMBER: US/10/101,388
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/711,562
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/164,886
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4653
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)..(4272)
US-10-101-388-2
```

```
Query Match          2.6%; Score 45; DB 9; Length 4653;
Best Local Similarity 49.4%; Pred. No. 0.1;
Matches 117; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
```

```
OY 1 ATGGCGAGAGACTACGATACCCCGCGGAGCGTGCAGGAGACCGGCTCTGGGG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3739 ATCGGCTACGGGCGCGGAGGCGGAGCGGAGGAGTGTGTGAGGCGGCGGAGGCG 3798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTGGCGCTGCTTCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3799 AACGGCGACCGGTTTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 AAGCTCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3859 GGGGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 ATCAAGCGGAGCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3919 CAGGCGCCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3975
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 15
US-10-101-388-1
; Sequence 1, Application US/10101388
; Patent No. US20020162142A1
; GENERAL INFORMATION:
; APPLICANT: Johal, Gurmukh S
; APPLICANT: Multani, Dilbag S
; TITLE OF INVENTION: GENES AND METHODS FOR MANIPULATION OF GROWTH
; FILE REFERENCE: 5718-81 (035718/205794)
; CURRENT APPLICATION NUMBER: US/10/101,388
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/711,562
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/164,886
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8036
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (371)
; OTHER INFORMATION: n at position 371 can be an a, g, c, or t.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (297)
; OTHER INFORMATION: n at position 297 can be an a, g, c, or t.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (400)
; OTHER INFORMATION: n at position 400 can be an a, g, c, or t.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (725)
; OTHER INFORMATION: n at position 725 can be an a, g, c, or t.
; NAME/KEY: unsure
; LOCATION: (856)
; OTHER INFORMATION: n at position 856 can be an a, g, c, or t.
US-10-101-388-1
```

```
Query Match          2.6%; Score 45; DB 9; Length 8036;
Best Local Similarity 49.4%; Pred. No. 0.13;
Matches 117; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

OY 1 ATGGCGAGAGACTACGATACCCCGCGGAGCGTGCAGGAGACCGGCTCTGGGG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7122 ATCGGCTACGGGCGCGGAGGCGGAGCGGAGGAGTGTGTGAGGCGGCGGAGGCG 7181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTGGCGCTGCTTCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7182 AACGGCGACCGGTTTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Qy 121 AAGCTGGCCATTGTTCCACACAGCGGACACAGAACCGCTGGCGGAGGCGCTGGAGAG 180
Db 7242 GGGGTGCAGCTGTCTGGGGGGGCGACGCGGATCGCATCGCGCGCTGTGTAAAG 7301
Qy 181 ATCAAGCGGAGCTGATGTGTGGGTTTCATCTCGCTGCTGCTGCGCGTACGCGAG 237
Db 7302 CAGCGGCGCATGCTGTGTGACGAGCGGCGCTGTGACGCGCGAGTCGAG 7358

Search completed: November 18, 2002, 15:35:06
Job time : 97 secs


```
Query Match      18 4%   Score 315.2   DB 4  
Best local similarity 64.6%   Pred. No. 1,9e-63  
Matches 486; Conservative 0; Mismatches 263; Indels 3; Gaps
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Oy 545 GCCTACGACGACAGAGCGTGTTCGTAAGGGGCAACTG--GGCTCCTCACACACCCTCC 601
 ||||| ||| |||
Db 2 GCCTACGCCACGAGACTTGCTTTGTGAGGCAGCATATATGCTCAACAAGTTCCAG 61

```

? RESULT 3
? US-09-183-959-13
? Sequence 13, Application US/09183959
? Patent No. 630332
?
? GENERAL INFORMATION:
?
? APPLICANT: Cahoon, Rebecca E.
? APPLICANT: Miao, Guo-Hua
? APPLICANT: Rafalski, J. Antoni
? APPLICANT: Tatamano, Graziana
? TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
? FILE REFERENCE: BB-1125
?
? CURRENT APPLICATION NUMBER: US/09/183,959
? CURRENT FILING DATE: 1998-11-02
? EARLIER APPLICATION NUMBER: 60/064,493
? EARLIER FILING DATE: No. 630332member 5, 1997
?
? NUMBER OF SEQ ID NOS: 20
?
? SOFTWARE: Microsoft Windows 95
?
? SEQ ID NO 13
?
? LENGTH: 338
?
? TYPE: DNA
?
? ORGANISM: Zea mays
?
? FEATURE:
?
? NAME/KEY: unsure
?
? LOCATION: (479)
?

```


Query Match 9.9%; Score 170; DB 4; Length 1831;

Best Local Similarity 49.0%; Pred. No. 4,9e-30; Matches 649; Conservative 0; Mismatches 615; Indels 60; Gaps 5;

```

Qy 25 CCGGCGGACGCGTCCGAGAGACGCGCTCCGAGGCGTGGCGTGGCTGCTTCGCGCTATG 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 CAGGGGGGCGTGGCGAGAGACGCGCTCCGAGGCGTGGCGTGGCGTGGCGTGGCGTGGCG 144
Qy 85 ATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
Qy 145 CGGACAGAGACGCGTGGCGAGGCGCTGGAGAGATCAAGACGCGAGCTGATGCTGCTG 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 ACCMAGGAGAGGCGATGCTGCGCGGCTGAGAGATCGGAGAGACTGATCTGCTGCTG 264
Qy 205 GGGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 GGAATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 324
Qy 261 -----CTCCGAGAGAGCGCGCATGCTGCG 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 TCTGCTCTTACAGCGCGCTTACATGCTGCTGCGAGAGGACTTACAGAGCTGCTG 384
Qy 289 CCGTGGAGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 CGGACAGAGAGCGCGACAGAGCGCGCTGCGACAGAGAGAGAGAGAGAGAGAGAGAGAG 444
Qy 337 TACTGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 CAGCTGCTGGCGAGGCGCATGAGACCTTTGTTGCTGAGAGAGAGAGAGAGAGAGAGAG 504
Qy 397 ATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 456
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 CGGTTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
Qy 457 AGCGTCTCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 TCCATGATCAAGATCTATAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 624
Qy 517 CAGTGGCAATGATCTGCGGCTGCTGCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAG 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 625 GAGGAATGAAAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 684
Qy 577 CACCTGGCGCTCTCCAGCAGCGCGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 AATGCTTCTCATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 744
Qy 631 CAGTCTTCTGAGTGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 CAATTCAGAGGCTCATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 802
Qy 691 GCGCATTTGTCGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 803 -CATATCACAGCTTACAGATTCATATGATTCATATATATATATATATATATATATATAT 861
Qy 751 GAGAGATTCAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 862 GATGATTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 921
Qy 811 CTCTTCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 922 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 981
Qy 871 ATCCCTTGTGTGTTGAAGCAAGCTGAGATGATGATGATGATGATGATGATGATGATGATG 930
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 982 CTGTGCTCTCTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1041
Qy 931 CAGGACCGGCGAGCGTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1042 GCTGA---GGCAAGAGCGCTTATGTTGGTCAACAATTAAGCTGAGATGATTAATTT 1098
```

```

Qy 991 TGGTTCACGCGCCCGAGCTGGTCTCTTTCATATACCTGACGCTGTTCCAGATGCG 1050
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1099 TGGTTCAGAAAGCTCGGAGTACTGCTGCTTATACAGTTCATTTTCATAGATGCT 1158
Qy 1051 TTTTCAGATGGCAGATTTGCTGAGACAGTGGCCAGCGCCGCTTGAAGAAATGCTTCAT 1110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1159 TTTGAGCTGGCAGATTTCTTATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
Qy 1111 ATGCAATGCGTCTGAGCATCATGAGAGTGTGCTGGGCTGCTTCAGTTCTCTGCTG 1170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1219 AAGCACTACTACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1278
Qy 1171 ACCTATATACCTTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1279 ACCTACAGACACTCCCGCTGATGATGATTTTCTGAGATGGCTCCCAAGTTCAAGAAA 1338
Qy 1231 TCCATCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1339 TCACGTGCTTGGAGAGAGTGAAGAGTGGTGCACAGCTGCTGCTGCTGCTGCTGCTG 1398
Qy 1291 AAGA 1294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1399 AGGA 1402
```

```

RESULT 8
US-09-183-959-17
; Sequence 17, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafaleki, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; NUMBER OF SEQ. ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ. ID NO. 17
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-17
```

Query Match 6.6%; Score 112.8; DB 4; Length 705;
Best Local Similarity 70.8%; Pred. No. 4,9e-17;
Matches 150; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

```

Qy 621 CTCTTCAGGAGTTCTCAGTGGTCCAGCAAGTGGAGTACCTTCAGCGGCGAGG 680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 CTCTTCGCGGAGTTCTCAGTGGTCCAGTGGAGCGAGAGTACTGCGCGCTGCGCACAG 234
Qy 681 CTTCATACAGCGGATTTGCGATATACAGCAAGTTGAGTCTTCACAAATGATACAGAG 740
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 CTCTTCAGGAGTCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294
Qy 741 GTCCATGAGAGAGAGTCAAGAGTGTGTTGGCATCAGGCTCCGCTGCTGCTGCTGCTG 800
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 GTCTCTGAGAGAGTCTCAAGTGTAGTGGGATCAGTCTCTGTGGCTTCTGCTGCTG 354
Qy 801 GATCCAGCGCTCTCTGATATATGAGAGAG 832
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 TCTCATCTTCTCTCTCTCAAGCTCAATGTA 386
```

RESULT 9
US-09-183-959-3
; Sequence 3, Application US/09183959
; Patent No. 6303332

[illegible]

```

RESULT 11
US-09-183-959-5
; Sequence 5, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Rafalino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 5
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (164)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (351)
; FEATURE:
;

```

REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 71380

FILING DATE: 07-JUN-1996
ATTORNEY/AGENT INFORMATION:

NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 026083/0193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-194-905-7

Query Match 2.6%; Score 45.2; DB 4; Length 6854;
Best Local Similarity 47.5%; Pred. No. 0.33;
Matches 134; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

16 GAGTACCCCGCGGACGCTGCCGAGACCCCTCCTGGGCGGTGGCGCTGCTTC 75
4937 GACGACCGGCGCGCATCGCTGCGCGTGGCGACCTGGGAGCTGGGCGAGCGC 4878
76 GCCGTATGATCATGTGTCCTCTCGAGACGCGCTCCACAGACTGGGCATTGG 135
4877 GTGGCGCTCGCGTGGGCGCGCGCTGCTGCGGTGCGAGGAGATGAGAGGGTTC 4818
136 TTCACAGCGGCAAGAGCGCGCTGGCGAGCGCTGGAGAGATCAAGCGGAGCTG 195
4817 CGGCGCGCGCTGGGAGACCTGGAGATGTCGCGCGGAGTCCGAGACCTGTCAG 4758
196 ATCGTGTGGGTTTCATCTCGCTCGCTCGCGTACGACAGACCACTCCGGGATA 255
4757 CACTCGCTGTCTCCCTGAGAGGGGCGGCGCGCTCGCGCTGATGACCTGGGC 4698
256 TGCATCTCCGAGAGCGCGCATCATGCGCGCGCTGACG 297
4697 TGCACCGCGCATGTGCGCCAGGACATGATGCGCTGGC 4656

RESULT 14
US-08-888-077A-18
Sequence 18, Application US/08888077A
Patent No. 6020143
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLIP, PETER H
APPLICANT: ROMMENS, JOHANNA M
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629

REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP CIP IV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2229 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 366..1712
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2226
OTHER INFORMATION: /note="np2"
US-08-888-077A-18

Query Match 2.6%; Score 44.4; DB 3; Length 2229;
Best Local Similarity 45.3%; Pred. No. 0.35;
Matches 162; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

24 CCGGCGGCGAGCGTCCGAGACGCGCTCGGCGGTGGCGCTGCTTGGCGCTCAT 83
1406 CCCAGGAGAGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1465
84 GATCATCTGCT 143
1466 CATCTTCTACAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1525
144 GCGGACAGAGAGCGCTGGCGAGGCGCTGAGAGAGATCAAGAGCGAGCTATGCTGT 203
1526 CACGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1585
204 GGGGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
1586 TGTGTTCAAGAGAGCGCTGCGCGCTCCCTCCATCTCATGACGTCGCTCATCTTTTA 1645
264 CGAGAGGCGCGCATCATGAGGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 323
1646 CTTTCCAGGAGACACTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1705
324 GTACAGACTACTACTGCGCCAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 381
1706 CATCTGAGGAGATGTGTGCGACAGCGTCAAGCTGCAAGGAAATTTTCATTGATGC 1763

RESULT 15
US-09-375-318-1
Sequence 1, Application US/09375318
Patent No. 6468791
GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Schellenberg, Gerard D.
TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BEERY LLP
STREET: 701 Fifth Ave, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,318
; FILING DATE: 16-Aug-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Verna, James M.
; REGISTRATION NUMBER: 33,287
; REFERENCE/DOCKET NUMBER: 920010.571C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2236 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-375-318-1

Query Match      2.6%; Score 44.4; DB 4; Length 2236;
Best Local Similarity 45.3%; Pred. No. 0.35;
Matches 162; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 24 CCCGCGCGGAGACGCTGCCGAGACGCCCTGCGGCGGCTGCGCTGCTGCGCGTCAT 83
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Db 1408 CCCAGGGAGAGAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTT 1467
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 84 GATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 143
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1468 CATCTCTACAGTGTGCTGTGGCAAGCGGCTGCCACGGGCGAGCGGAGCTGGAATAC 1527
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 144 GCGGCAAGAAGACGCTGCGGAGAGCGCTGGAGAGATCAAAAGCGAGCTGATGCTGCT 203
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1528 CAGCGTGGCGCTTGTGCTGCGCATCTCATTTGCTGTGCTGACCTCTGCTGCTGCT 1587
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 204 GGGGTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1588 TGTGTTCAAGAAGAGCGCTGCCCTCCCTCCATTCATACGTTGCGGCTCATCTTTTA 1647
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QY 264 CGAAGAAGCGCCGAGCATCATGCGGCGCTGACGCTGCCCTGCTGCTGCTGCTGCTGCT 323
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Db 1648 CTTTTCACAGGACCAACCTGGTGGCGCGTTCAATGACACCTGGGCTCCCATCAGCTCTTA 1707
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QY 324 GTACAAAGACTACTACGCGCAAAAGGCAAGGTGCTGCTAATGTCCACGGGCGAGC 381
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Db 1708 CATCTGAGGAGCATGTGTGCTCACAGGCTGCAAGGAAATTTTCATTGTGATGC 1765
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Search completed: November 18, 2002, 14:37:44
Job time : 98 secs

Matches 636; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

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QY 281 TCATGCGGCTCGAGCCTCCCTCGTTCGTCAAGACAGTACAAAGTACTACT 340
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    |||||
QY 341 GCGCCAAAAGGCGAAGTGTGCTATGTCCAGCGGAGCTTGACACAGCTCCACATAT 400
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Db 62 GCGC---GGAGGGCAAGGTGGGCTCATGTCCAGGGGAGCTTGACACAGCTGCT 118
    |||||
QY 401 TCATCTGTGCTGCGGCTTCCATGTCACTACAGGCTTATACATAGCTTAAAGC 460
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Db 119 TCATCTGTGCTGCGGCTTCCATGTCACTACAGGCTTATACATAGCTTAAAGC 178
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QY 461 GTCTCAAAATGAGACATGTGAGAAATGGAGACAGACCCGCTCTTGGAATACAT 520
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Db 179 GTCTCAAAATGAGAAACATGTGAGAAATGGAGACAGACCCGCTCTTGGAATACAT 238
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QY 521 TCGCAATGATCTGCGGCTTCCGCTTCAGGACACAGAGCTGTTGTAAGCGGAC 580
    |||||
Db 239 TCGCAATGATCTGCGGCTTCCGCTTCAGGACACAGAGCTGTTGTAAGCGGAC 298
    |||||
QY 581 TGGGCTCTTCAGACAGCCCGGAGTACAGATGGGTGGTGGCTTTCAGGACATTTCA 640
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Db 299 TGGGCTCTTCAGACAGCCCGTGGCATCAGATGGGTGGTGGCTTTCAGGACATTTCA 358
    |||||
QY 641 GGTGGTACCAAGGTGAGTACCTACCTGAGGCGGAGGCTTCATCAAGCGGCAATTTGT 700
    |||||
Db 359 GGTGGTACCAAGGTGAGTACCTACCTGAGGCGGAGGCTTCATCAAGCGGCAATTTGT 418
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QY 701 GCGATTAACAGCAAGTTGCACTTCACAGTACATCAAGAGTTCATGAGAGACATTTCA 760
    |||||
Db 419 CCGAAACAGCAAGTTGCACTTCACAGTACATCAAGAGTTCATGAGAGACATTTCA 478
    |||||
QY 761 AAGTGTGCTGGCATAGCTCCGCTGGTGGTGGGACATCTCAGGCTTCTCTTG 820
    |||||
Db 479 AAGTGTGCTGGCATAGCTCCGCTGGTGGTGGGACATCTCAGGCTTCTCTTG 538
    |||||
QY 821 ATATTGACGGGATCGCAGCCTCCTACCTGATTTCTTTCATCCCTCTGTCATCTTGT 880
    |||||
Db 539 ACATCAATGAGGGGTGGACGCTCATCTGATTTCTTTCATCCCTCTGTCATCTTGT 598
    |||||
QY 881 GTTTGGAACCAAGCTGAGATGATCATGAGATGAGATGGCCCTGGAATCCAAAGACGG 940
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Db 599 GTTTGGAACCAAGCTGAGATGATCATGAGATGAGATGGCCCTGGAATCCAAAGACGG 658
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QY 941 CGAGCGTATCAAGGGGCGCCGCTGGTGAAGCCAGCAACA 982
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Db 659 CGAGCGTATCAAGGGGCGCCGCTGGTGAAGCCAGCAACA 700
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RESULT 3

BJ482842/c 681 bp mRNA linear EST 23-MAY-2002
LOCUS BJ482842 K. Sato unpublished cDNA library, strain H602 adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone bah4117 3', mRNA sequence.
ACCESSION BJ482842
VERSION BJ482842.1 GI:21161300
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 681)
REFERENCE
AUTHORS Sato, K., Saisho, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shinn-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshinn@genetics.nig.ac.jp.
Location/Qualifiers

FEATURES

source

1. .681
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah41117"
/clone_jib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 132 a 184 c 193 g 171 t 1 others
ORIGIN

Query Match 34.2%; Score 584.6; DB 13; Length 681;

Best Local Similarity 91.2%; Pred. No. 8.3e-105;

Matches 620; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 1021 TTCATACCTGACGCTGTTCCAGATGCGTTTCAGATGGACATTTGCTGACAGTG 1080
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Db 681 TTCATACCTGACGCTGTTCCAGATGCGTTTCAGATGGACATTTGCTGACAGTG 622
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QY 1081 GCGACGCGCGCTTGAGAAATGCTCCATATGACATCGGCTGAGCATCATGAGGTG 1140
    |||||
Db 621 GCGACGCGCGCTTGAGAAATGCTCCATATGACATCGGCTGAGCATCATGAGGTG 562
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QY 1141 GTGCTGGGCTGCTCTTCAGTCTCTGCACTATATACCTTCCCTCTAGCGCTC 1200
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QY 1201 GTCAACAGATGGGATGCAACATGAGAGGTCTCTGAGAGAGAGCGCAAGGCG 1260
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Db 501 GTCAACAGATGGGATGCAACATGAGAGGTCTCTGAGAGAGAGCGCAAGGCG 442
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QY 1261 CTGACCACTGCGGGAACAGCGCCAGAGAAAGAGTCCGAGACAGGACATGCTG 1320
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Db 441 CTGACCACTGCGGGAACAGCGCCAGAGAAAGAGTCCGAGACAGGACATGCTG 382
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QY 1321 ATGCGGAGATGATCGGCGAGCGAGCGCCAGCGGACGTCGCGCATGCTAGCGCG 1380
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Db 381 ATGCGTCAAGTATGCGGCGAGCGAGCGGAGCGCGCATGCGCGCATGCGCGAGCG 322
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QY 1381 GCTTCGTCACCGGTGCACTGCTTCAACAGGAGATGGAGCGTCCGAGATGCCAGAGC 1440
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Db 321 GCGTCATACCGGTGCACTGCTTCAACAGGAGATGGAGCGTCCGAGATGCCAGAGC 262
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QY 1441 GCGCGGACCTCGGCAAGAGCACTGAGAGAGCTTAGGAGATGATACCCGTTGTGGGCG 1500
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Db 261 GCGCGGACCTCGGCAAGAGCACTGAGAGAGCTTAGGAGATGATACCCGTTGTGGGCG 202
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QY 1501 CATCGGTCGACAGACTAATATCTGTCGACAGGCGGAGTCTCTTCGTCGCGACTC 1560
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Db 201 CATCGGTCGACAGACTAATATCTGTCGACAGGCGGAGTCTCTTCGTCGCGACTC 142
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QY 1561 GATCGGACATCCCGAGCGCAGATTTTCTTCAGCGCAGGAGTGAACAAAGTTATATGAT 1620
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Db 141 GAACCGACATCCCGAGCTGCAAGATTTTCTTCAGCGCAGGAGTGAACAAAGTTCTGTAT 82
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QY 1621 TGAGTATGTCGAATGATATAGCCACATAGAGATGCTATGTTGTCATTAAGAAATGA 1680
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Db 81 TCATGTTAGTCAATGTATATAGCCACATAGAGATGATGATGTTGTCATTAAGAAATGA 22
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QY 1681 ATTTTTCAGTGAAGCAAAA 1700
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Db 21 ATTTTTCAGTGAAGCAAAA 2
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RESULT 4

AV945501/c 669 bp mRNA linear EST 18-JAN-2002
LOCUS AV945501 K. Sato unpublished cDNA library, strain H602 adult,
DEFINITION AV945501 K. Sato unpublished cDNA library, strain H602 adult,

QY	1019	TCGTATACACCTGAGCGCTGTTCCAGAGATGCGTTTCAGATGGGCAATTCGTGGACAG	1078
Db	667	TCCTATACACCTGACCTGTTTCCAGAACGCGTTTCAGATGGCGCATTTTGTGGACAG	608
QY	1079	TGGCAGCGCCGGCTTGAAGAAATGCTTCCATATGACATCGGTGTGACATCATAGC	1138
Db	607	TGGCAGCGCCGGCTTGAAGAAATGCTTCCACACAGCATGATCGGGTGTAGCATCATAGAG	548
QY	1139	TGCTGCTGGGGCTGGCTCTTCAAGTTCCTGACATATATATCACTTTCCCTGTAGCGGC	1198
Db	487	TCCTCACACAAATGGGATCAAAATGAAGAGGTTCATCTTTCAGAGAGACGTCACAG	428
QY	1259	CGCTGACCAACTGGCGGAGACAGCGCCCAAGAGAGAAAGGTCCGAGACACGAGCATGC	1318
Db	427	CGCTCACCAATGGCGGAGACAGCGCCCAAGAGAGAAAGGTCCGAGACACGAGCATGC	368
QY	1319	TGATGGCGCATATATATGCGGAGACGGAGCGCCACCGAGCATGTCGGCATGCTTAGCC	1378
Db	367	TGATGGCTCAATGATATGCGGAGACCGAGCCAGCGCTGTGCGCATGTCGCGAGCC	308
QY	1379	GGGCTTTCGTCACTCGGTGCACCTGCTTTCACAAAGGGCATGGAGCGTCCGACATCCCA	1438
Db	307	GGGGCTCAATCACTCGGTGCACCTGCTTTCACAAAGGGCATGGAGCGTCCGACATCCCA	248
QY	1439	GGCGCGCAACCTCGCAGAGGACCATGAGAGAGGTAGGAGCATGTAACCGGTTGTGGTG	1498
Db	247	GGCGCGCAACCTCGCAGAGGACCATGAGAGAGGTAGGAGCATGTAACCGGTTGTGGTG	188
QY	1499	CGCATCCCGTGCACAGACTAAATCCTGCTGACAGGCGGAGTGGCTCTCTTGTGGCAC	1558
Db	187	CGCAGCCGGTGCACAGACTAAATCCTGACAGAGAGAGGTGCGCTCATCATCGGCC	128
QY	1559	TGCATCGCAATCCCGAGCGCAGATTTTTCCTTCAGCCAGGGATGAGACAAGTTTAT	1618
Db	127	TGCAGCCGCAATCCCGAGCGCAGATTTTTCCTTCAGCCAGGGATGAGACAAGTTTCTG	68
QY	1619	ATTGATGTTAGTCCATATGTTATAGCCAACTAGAGTGTGATGCTATTAAGAAAT	1678
Db	67	ATTCAATGTTAGTCCATATGTTATAGCCAACTAGAGTGTGATGCTATTAAGAAAT	9
QY	1679	GAATTTT 1686	
Db	8	CAATTTT 1	
RESULT 7			
LOCUS	BU483757/c	669 bp	mRNA
DEFINITION	BU483757 K. Sato unpublished cDNA library, strain H602 adult,		linear EST 23-MAY-2002
ACCESSION	BU483757	headling stage top three leaves	Hordeum vulgare subsp. spontaneum
VERSION	BU483757.1	cdna clone bh47c15 3', mRNA sequence.	
KEYWORDS	EST.		
SOURCE	Hordeum vulgare subsp. spontaneum.		
ORGANISM	Hordeum vulgare subsp. spontaneum		
REFERENCE	Authors		
TITLE	Sato, K., Saitoh, D. and Takeda, K.		
JOURNAL	Barley EST sequencing project in NIG and Okayama Univ		
COMMENT	Unpublished (2002)		
	Contact: Tadasu Shin-1		

National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856


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ACCESSION      BJ479219
VERSION        BJ479219.1  GI:21157697
KEYWORDS
SOURCE         Hordeum vulgare subsp. spontaneum.
ORGANISM       Hordeum vulgare subsp. spontaneum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
                ; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 636)
AUTHORS        Sato, K., Saitoh, D. and Takeda, K.
TITLE          Barley EST sequencing project in NIG and Okayama Univ
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasi Shin-i
                Center for Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshini@genes.nig.ac.jp.
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BASE COUNT      131 a 176 c 164 g 165 t
ORIGIN
Query Match
Best Local Similarity 94.3%; Score 476; DB 13; Length 636;
Matches 494; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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RESULT 13
AV835197
LOCUS
DEFINITION     AV835197 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
                spontaneum top three leaves adult, heading stage Hordeum vulgare
                subsp. spontaneum cDNA clone bah26013, mRNA sequence.
ACCESSION      AV835197.1  GI:14527286
VERSION
KEYWORDS
SOURCE         Hordeum vulgare subsp. spontaneum.
ORGANISM       Hordeum vulgare subsp. spontaneum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
                ; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 605)
AUTHORS        Sato, K.
TITLE          Barley EST sequencing project in NIG and Okayama Univ
JOURNAL        Unpublished (2001)
COMMENT        Contact: Kazuhito Sato
                Research Institute for Bioresources
                Okayama University, Barley Germplasm Center
                Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
                Email: kazsato@rib.okayama-u.ac.jp;
                URL: http://www.rib.okayama-u.ac.jp/barley/
                Sato, K., Saitoh, D., Takeda, K., Shin, I. T. and Kohara, Y. Direct
                submission;
                database: http://www.shigen.nig.ac.jp/Barley/Barley.html.
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        /cultivar="H602"
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        /clone="bah26013"
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        stage"
        /tissue_type="top three leaves"
        /dev_stage="adult, heading stage"

BASE COUNT      131 a 188 c 163 g 122 t 1 others
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Query Match
Best Local Similarity 87.8%; Score 458; DB 10; Length 605;
Matches 324; Conservative 0; Mismatches 66; Indels 7; Gaps 2;

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OY 632 AGTTCTTCAGTGGTCCACCAAGGTGAGTACCTCCCTGAGGGCAGGCTTCATCAAGC 691
 DB 429 AGTCTTCAGTCAAGTCAACCAAGGTGAGTACCTGACCTTGAAGGCGAGCTTCATCAAGC 488
 OY 692 CGCATTTGTGCGATTAACGACGAAGTTGCACCTCCACAAAGTACATCAAGAGTCCATGAGG 751
 DB 489 CGCATTTGTGCGCAAAACAGCAAGTTGCACCTCCACAAAGTACATCAAGAGTCCATGAGG 548
 OY 752 AGCAATTCAAAGTGGTGGTGCATGACCTCCGCGTGGTGGTGGAGTCCCTCA 808
 DB 549 ACCACTTCAAGGTGCTGCTCGGCATCAGCCTCCCGCTGGGGGTGGCGATCTCTCA 605

RESULT 14
 BG904891/c 490 bp mRNA linear EST 05-JUN-2001
 LOCUS Talr135F04F Talr1 Trilicium aestivum cDNA clone Talr135F04 3',
 DEFINITION mRNA sequence.

ACCESSION BG904891 GI:14312567
 VERSION BG904891
 KEYWORDS EST.
 SOURCE bread wheat.

ORGANISM Trilicium aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 : Triticeae; Trilicium.

REFERENCE 1 (bases 1 to 490)
 Cloutier, S., Dong, G. and Walsh, A.
 Wheat functional genomics - Thatcher Lr1 cDNA library
 Unpublished (2001)
 CONTACT: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-food Canada
 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@em.agr.ca

was cloned directionally, not all sequences generated with reverse
 primer were from the 3' end (same with forward primer and 3' end).
 Average insert size is >2.2 kb
 Plate: 135 row: F column: 04
 Seq primer: M13 Forward.

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 Location/Qualifiers
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 /cultivar="Thatcher Lr1"
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 /clone="Talr135F04"
 /clone_1lb="Talr1"
 /tissue_type="leaf tissue"
 /dev_stage="14 Days old"
 /lab_host="E. coli XL0LR"
 /note="Vector: Lambda ZapII; mass excised in plasmid
 vector pBK-CMV (Stratagene); Site 1: EcoRI; Site 2: XhoI;
 mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
 inoculation with leaf rust pathogen Puccinia tritici
 race BB5 carrying the avirulence gene AVR1."

BASE COUNT 90 a 143 c 130 g 127 t
 ORIGIN
 Query Match 26.5%; Score 453.2; DB 12; Length 490;
 Best Local Similarity 95.3%; Pred. No. 5.4e-79;
 Matches 467; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 1202 TCACACAGATGGAGTGAAGAGGTCATCTTCAGCAGCAGCAGCGCCAGGCGC 1261
 DB 490 TCACACAGATGGAGTGAAGAGGTCATCTTCAGCAGCAGCAGCGCCAGGCGC 431
 OY 1262 TGACCACTGGCGCAACAGCGCAAGAGAGTCCGAGACGACGACATGCTGA 1321
 DB 430 TGACCAACTGGCGCAACAGCGCAAGAGAGTCCGAGACGACGACATGCTGA 371
 OY 1322 TGGCGCAGATGATGCGCAGCGCAGCGCCAGGCGACGTCGCGATGCTGACGCGG 1381

DB 370 TGGCGCAGATGATGCGCAGCGCAGCGCCAGCGGCGGCGTCCCATGCTTACGCGG 311
 OY 1382 CTTCGACCGGTCGACACCTGCTTCACAAAGGGCATGGGACGTCGACGATCCCGAGAGC 1441
 DB 310 GCTGTCGCGCAGTGCACCTGCTTCACAAAGGGCATGGGACGTCGACGATCCCGAGAGCA 251
 OY 1442 CGCCGACCTGCGCAAGGACCATGAGAGAGGCTAGGACATGTACCCGTTGTGTGGCGC 1501
 DB 250 CGCCACACTGCGCAAGGCGCCATGAGAGGCTAGGACATGTACCCGTTGTGTGGCGC 191
 OY 1502 ATCCCGTCACAGATGAATATCTGCTGACAGCGGAGTGGTCTCTGTCGCGACTCG 1561
 DB 190 ATCCAGTGCACAGACTGAATATCTGCTGACAGGAGTGGTCTCTGTCGCGACTCG 131
 OY 1562 ATGCGACATCCCGACGCGCAGATTTTCTTCAGCGCAGGATGAGCAAGTTATGCTAT 1621
 DB 130 AGTGTGACATTCCTCCGCGCGAGATTTTCTTCAGCGCAGGATGAGCAAGTTGCTGAT 71
 OY 1622 GATGTTAGTCCATGATAGCCACATAGATGATGATTCGTACAAATAGAAATAGAA 1681
 DB 70 GATGTTAGTCCATGATAGCCACATAGATGATGATTCGTACAAATAGAAATAGAA 11
 OY 1682 TTTTCTACTG 1691
 DB 10 ATTTTTCCTG 1

RESULT 15
 BEA19320 613 bp mRNA linear EST 24-JUL-2000
 LOCUS WMR06.F5R000101 TREC WMR wheat Root Library Trilicium aestivum cDNA
 DEFINITION clone WMR06.F5, mRNA sequence.

ACCESSION BEA19320
 VERSION BEA19320.1 GI:9417166
 KEYWORDS EST.
 SOURCE bread wheat.

ORGANISM Trilicium aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 : Triticeae; Trilicium.

REFERENCE 1 (bases 1 to 613)
 Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier,
 S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
 Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,
 Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
 Pechion, N., Qalset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
 Sorrells, M., Warburton, M. and Wenzel, G.
 International Triticeae EST Cooperative (TREC): Production of
 Expressed Sequence Tags for Species of the Triticeae
 Unpublished (2000)

CONTACT: Schuch W
 Zeneca Wheat Improvement Centre, Norwich Research Park
 Colney Lane, Norwich NR4 7UH UNITED KINGDOM
 Tel: 44 1603 250 2600
 Fax: 44 1603 250 699
 Email: wolfgang.schuch@aguk.zeneca.com
 International Triticeae EST Cooperative (TREC)
 http://wheat.pw.usda.gov/genome.

FEATURES
 source
 Location/Qualifiers
 1..613
 /organism="Trilicium aestivum"
 /cultivar="Novosibirskaya 67"
 /db_xref="taxon:4565"
 /clone="WMR06.F5"
 /clone_1lb="TREC WMR wheat Root Library"
 /tissue_type="root"
 /note="M13 Reverse sequencing primer used for 5' end of
 clone."

BASE COUNT 121 a 180 c 150 g 159 t 3 others
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 Query Match 24.9%; Score 426; DB 10; Length 613;
 Best Local Similarity 94.0%; Pred. No. 1.1e-73;

OY 1322 TGGCGCAGATGATGCGCAGCGCAGCGCCAGGCGACGTCGCGATGCTGACGCGG 1381

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 14:36:08 ; Search time 67 Seconds

(without alignments)
1062.027 Million cell updates/sec

Title: US-09-857-896A-32

Perfect score: 2784

Sequence: 1 MAEDYEPKARLPTPSWA.....VSSSLADIPADPSFSQG 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2784	100.0	534	21 AAB01805	Wheat Mlo homologue
2	2777	99.7	534	22 AAY26967	Wheat Mlo fungal r
3	2777	99.7	534	22 AAB31251	Amino acid sequenc
4	2740	98.4	534	20 AAY26966	Wheat Mlo fungal r
5	2740	98.4	534	22 AAB31250	Amino acid sequenc
6	2680	96.3	534	20 AAY26968	Wheat Mlo fungal r
7	2680	96.3	534	22 AAB31252	Amino acid sequenc
8	2434	87.4	533	19 AAM59442	Hordeum vulgare ML
9	2434	87.4	533	21 AAB03401	Barley Mlo protein
10	2428	87.2	533	19 AAM59443	Hordeum vulgare ML

11	1946	69.9	544	19 AAM59445	Hordeum vulgare ML
12	1737.5	62.4	536	19 AAM59444	Oryza sativa MLO P
13	1276.5	45.9	573	20 AAY26970	Arabidopsis thalia
14	1276.5	45.9	573	21 AAG35698	Arabidopsis thalia
15	1276.5	45.9	573	22 AAB31254	Amino acid sequenc
16	1241	44.6	585	21 AAB03404	Arabidopsis thalia
17	1201	43.1	515	20 AAY4139	Zea mays SCLB pro
18	1201	43.1	515	21 AAY44605	Maize MLO6 protein
19	1195	42.9	565	21 AAY44602	Maize MLO2 protein
20	1160.5	41.7	569	20 AAY26969	Arabidopsis thalia
21	1160.5	41.7	569	22 AAB31253	Amino acid sequenc
22	1149.5	41.3	593	20 AAY26972	Arabidopsis thalia
23	1149.5	41.3	593	22 AAB31256	Amino acid sequenc
24	1147	41.2	521	21 AAB01797	Wheat Mlo homologue
25	1107	39.8	542	21 AAB03402	Arabidopsis thalia
26	1085.5	39.0	511	21 AAG35699	Arabidopsis thalia
27	1069	38.4	530	21 AAB01795	Soybean Mlo homolo
28	991	35.6	482	21 AAG35700	Arabidopsis thalia
29	962	34.6	506	21 AAB01794	Soybean Mlo homolo
30	958	34.4	187	21 AAB01793	Soybean Mlo homolo
31	932.5	33.5	526	19 AAM59446	Arabidopsis thalia
32	932.5	33.5	526	21 AAB03405	Arabidopsis thalia
33	927.5	33.3	526	22 AAB31255	Amino acid sequenc
34	925	33.2	492	21 AAB01808	Wheat Mlo homologue
35	924.5	33.2	526	20 AAY26971	Arabidopsis thalia
36	901	32.4	450	21 AAB01798	Wheat Mlo homologue
37	888	31.9	492	21 AAY44607	Maize MLO8 protein
38	887.5	31.9	492	20 AAY44135	Zea mays SCLB pro
39	796.5	28.6	496	21 AAY44782	Maize MLO3 protein
40	796.5	28.6	496	22 AAU00505	Maize disease resi
41	770.5	27.7	499	21 AAY44806	Maize MLO7 protein
42	752	27.0	224	21 AAY44601	Maize MLO1 protein
43	745.5	26.8	264	20 AAY44140	Zea mays SCLB pro
44	736	26.4	509	20 AAY44138	Zea mays SCLB pro
45	735	26.4	509	21 AAY44603	Maize MLO4 protein

ALIGNMENTS

RESULT 1
ID AAB01805
AC AAB01805:
XX 27-OCT-2000 (first entry)
XX Wheat Mlo homologue putative protein sequence #4.
XX DE Wheat Mlo homologue; disease resistance.
XX KW Wheat; Mlo homologue; disease resistance.
XX OS Triticum aestivum.
XX PN WO200036110-A2.
XX PD 22-JUN-2000.
XX PF 17-DEC-1999; 99WO-US30181.
XX PR 18-DEC-1998; 98US-0112737.
XX PA (DDPO) DU PONT DE NEMOURS & CO E I.
XX Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
WPI: 2000-431590/37.
XX N-PSDB: AAA52715.
XX New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT creating transgenic plants with altered levels of disease resistance -
XX Claim 10; Page 64-66; 79pp; English.

XX The present sequence is a putative protein sequence for a Mlo homologue
CC from wheat. Its coding sequence was identified by searching a root and
CC leaf cDNA library for sequences encoding proteins similar to Mlo from
CC Hordeum vulgare (barley) and Arabidopsis thaliana. Mlo confers resistance
CC to Erysiphe graminis f. sp. hordei upon the plant, and its inactivation
CC leads to the priming of disease resistance even if the pathogen is not
CC present. The gene and protein can be used to create transgenic plants
CC which have increased disease resistance, as well as allowing researchers
CC to find other resistance-conferring genes and proteins.

XX Sequence 534 AA:

Query Match 100.0%; Score 2784; DB 21; Length 534;
Best Local Similarity 100.0%; Pred. No. 6,2e-289;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDYEYPARTLPETPSMAVALVFAVMITVSVLEHALHKLGHMFKRRKNALEALEK 60
DB 1 MAEDYEYPARTLPETPSMAVALVFAVMITVSVLEHALHKLGHMFKRRKNALEALEK 60
QY 61 IKAELMLVGFISLLAVTODPISGICISEKAASIMRPSLPPGSVKSKYKDYCAKKGKV 120
DB 61 IKAELMLVGFISLLAVTODPISGICISEKAASIMRPSLPPGSVKSKYKDYCAKKGKV 120
QY 121 SLMTSGSLHQLHIFIVLAVFHYTVSYIIMASRLKMTWKKEETASLEYOFPANDPAR 180
DB 121 SLMTSGSLHQLHIFIVLAVFHYTVSYIIMASRLKMTWKKEETASLEYOFPANDPAR 180
QY 181 FRFTHOTSPVKRHLGLSTSPGIRMVVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
DB 181 FRFTHOTSPVKRHLGLSTSPGIRMVVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
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DB 241 FHKYIKRSMEDDFKVVVGISLPLMCVAITLFLDIDIGITLWISFPIVYLICVGTKE 300
QY 301 MIIMEMALEIODRASVIKGAPEVPSNKFEMFHRPDWVLFHILTLFQNAFQMAHFVMTV 360
DB 301 MIIMEMALEIODRASVIKGAPEVPSNKFEMFHRPDWVLFHILTLFQNAFQMAHFVMTV 360
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DB 361 ATPGLKCFNHIGLSIMKYVLGLAQFLCSYITFPPLVALVTOMGSNMKRSIFDEQTAKA 420
QY 421 LTNMRNTAKKVKVRODMLMAQIMIGDATPSRGTSPMPSRASSPVHLHLKMGSRDDPOS 480
DB 421 LTNMRNTAKKVKVRODMLMAQIMIGDATPSRGTSPMPSRASSPVHLHLKMGSRDDPOS 480
QY 481 APTSPRTMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDADIPSADEFSFSG 534
DB 481 APTSPRTMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDADIPSADEFSFSG 534

RESULT 2

AAI26967 standard; Protein: 534 AA.

AAI26967:

21-DEC-1999 (first entry)

Wheat Mlo fungal resistance protein Trm102.

Consensus: resistance: fungus; pathogen: wheat; cell wall: apposition;
papillae; contact site; callose; carbohydrate; phenol; transgenic plant;
Mlo; Erysiphe graminis; powdery mildew.

Triticum sp.

Key Location/Qualifiers
Misc-difference 168 /label= unknown

/note= "encoded by GTC"

XX WO9447552-A2.
XX 23-SEP-1999.
XX 17-MAR-1999; 99WO-Ep01779.
XX 17-MAR-1998; 98US-0042763.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-EREINDUNGEN VERW GES MBH.
XX Salmeron JM, Welislo LJ, Strawn LJ, Kramer CM;
XX WPI: 1999-571820/48.
XX N-PsDB; AA30410.

XX New proteins useful for generating transgenic plants resistant to
XX fungal infection -
XX Claim 2; Page 63-65; 102pp; English.
XX This sequence represents the wheat fungal resistance protein Trm102,
XX which confers resistance to fungal pathogens by stimulating the formation
XX of large cell wall appositions, designated papillae, at the contact site
XX with the fungal pathogen. These papillae mainly contain callose, but
XX also contain carbohydrate, phenols and proteins and are used to prevent
XX penetration of the fungal hyphae into the plant. The new Mlo sequences
XX are used to generate transgenic plants resistant to fungal pathogens,
XX especially Erysiphe graminis (powdery mildew).

XX Sequence 534 AA:

Query Match 99.7%; Score 2777; DB 20; Length 534;
Best Local Similarity 99.6%; Pred. No. 3,5e-288;
Matches 532; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAEDYEYPARTLPETPSMAVALVFAVMITVSVLEHALHKLGHMFKRRKNALEALEK 60
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DB 61 IKAELMLVGFISLLAVTODPISGICISEKAASIMRPSLPPGSVKSKYKDYCAKKGKV 120
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DB 121 SLMTSGSLHQLHIFIVLAVFHYTVSYIIMASRLKMTWKKEETASLEYOFPANDPAR 180
QY 181 FRFTHOTSPVKRHLGLSTSPGIRMVVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
DB 181 FRFTHOTSPVKRHLGLSTSPGIRMVVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
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QY 361 ATPGLKCFNHIGLSIMKYVLGLAQFLCSYITFPPLVALVTOMGSNMKRSIFDEQTAKA 420
DB 361 ATPGLKCFNHIGLSIMKYVLGLAQFLCSYITFPPLVALVTOMGSNMKRSIFDEQTAKA 420
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DB 421 LTNMRNTAKKVKVRODMLMAQIMIGDATPSRGTSPMPSRASSPVHLHLKMGSRDDPOS 480
QY 481 APTSPRTMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDADIPSADEFSFSG 534
DB 481 APTSPRTMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDADIPSADEFSFSG 534

RESULT 3

AAB31251 standard; Protein: 534 AA.

ID AAB31251

AC AAB31251

XX 20-APR-2001 (first entry)

DE Amino acid sequence of the wheat M10 protein Trm102.

KM wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;

KW powdery mildew; M10; cell wall apposition; transgenic plant.

XX Triticum sp.

FH Key Location/Qualifiers

FT Misc-difference 168 /note="unspecified amino acid encoded by GYC"

XX WO200078799-A2.

PD 28-DEC-2000.

PE 16-JUN-2000; 2000WO-EP05576.

PR 18-JUN-1999; 99US-0336112.

PA (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;

XX Vernooij BR, Levin JZ, Hefetz PB, Patton DA, Que Q;

DR WPL: 2001-112311/12.

DR N-PSDB; AAF24584.

XX Novel polynucleotide which encodes M10 protein from wheat, useful for

XX producing fungal resistant plants, in particular wheat plant -

PS Claim 12; Page 94-96; 128pp; English.

XX The present sequence represents a M10 protein. M10 proteins given

CC resistance to fungal pathogens which infect living epidermal plant cells.

CC M10 proteins give proteins resistance to fungal pathogens, especially

CC Erysiphe graminis (powdery mildews). In barley, mutations at the M10

CC locus are responsible for a plant resistant pathotype. The mechanism

CC of M10 resistance involves the formation of large cell wall appositions,

CC called papillae, at pathogen contact sites. Papillae mainly contain

CC callose, but also carbohydrates, phenols and proteins. Polynucleotides

CC encoding M10 proteins are useful for making transgenic plants,

CC preferably wheat, which are resistant to fungal pathogens.

SQ Sequence 534 AA;

Query Match 99.7%; Score 2777; DB 22; Length 534;

Best Local Similarity 99.6%; Pred. No. 3.5e-288;

Matches 532; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAEDYEPPARTLPETPSNAVALFAVAVIIVSYLLEHALHKGHMFHKKHNALEALEK 60

OY 61 IKALMLVGFISLLAVTODPISGICISEKASIMRPSLPGSVKSKYKDYCAKKGKV 120

DB 61 IKALMLVGFISLLAVTODPISGICISEKASIMRPSLPGSVKSKYKDYCAKKGKV 120

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DB 121 SLWSTGSLHOLHMFIFVLAVFHVITSVIMALSLKMKRWKKEETYSLEYOFPANPAR 180

OY 181 FRFTHOTSFWKRLGLSSTPGIRWVVAFFROFPRSVTKYDYLLTRAGFINAHLSHNSKFD 240

DB 181 FRFTHOTSFWKRLGLSSTPGIRWVVAFFROFPRSVTKYDYLLTRAGFINAHLSHNSKFD 240

OY 241 FHKTIKSMEDDDKRVVVGISLPLKCAVAILTLFDIDIGITWTWISPIPVILLCVGTLE 300

DB 241 FHKTIKSMEDDDKRVVVGISLPLKCAVAILTLFDIDIGITWTWISPIPVILLCVGTLE 300

OY 301 MIMEMALEIODRASVYKGAPEVPSNKFHFHPRDVLFFIHLTLFQNAFQMAHFVTV 360

DB 301 MIMEMALEIODRASVYKGAPEVPSNKFHFHPRDVLFFIHLTLFQNAFQMAHFVTV 360

OY 361 ATPGLKCFHMHGSLIMKVLGLAQFLCSTIFPLALVTOGSMKRSIFDQTKA 420

DB 361 ATPGLKCFHMHGSLIMKVLGLAQFLCSTIFPLALVTOGSMKRSIFDQTKA 420

OY 421 LTNNRNTAKKKKVRDTMLMAOMTGDATPSKGTSPMPSRASPVLHLKMGCRSDPQS 480

DB 421 LTNNRNTAKKKKVRDTMLMAOMTGDATPSKGTSPMPSRASPVLHLKMGCRSDPQS 480

OY 481 APTSPRTMEAROMKPYVVAHPRHLNPADRRRSVSSALDADIPSDPSFSG 534

DB 481 APTSPRTMEAROMKPYVVAHPRHLNPADRRRSVSSALDADIPSDPSFSG 534

RESULT 4

AAY26966 standard; Protein: 534 AA.

ID AAY26966

AC AAY26966

DT 21-DEC-1999 (first entry)

DE Wheat M10 fungal resistance protein Trm101.

KM Consensus: resistance; fungus; pathogen; wheat; cell wall; apposition;

KW papillae; contact site; callose; carbohydrate; phenol; transgenic plant;

KM M10; Erysiphe graminis; powdery mildew.

OS Triticum sp.

PN WO9947552-A2.

PD 23-SEP-1999.

PE 17-MAR-1999; 99WO-EP01779.

PR 17-MAR-1998; 98US-0042763.

PA (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;

DR WPL: 1999-571820/48.

DR N-PSDB; AAZ30409.

XX New proteins useful for generating transgenic plants resistant to

XX fungal infection -

PS Claim 2; Page 58-60; 102pp; English.

XX This sequence represents the wheat fungal resistance protein Trm101,

CC which confers resistance to fungal pathogens by stimulating the formation

CC of large cell wall appositions, designated papillae, at the contact site

CC with the fungal pathogen. These papillae mainly contain callose, but

CC also contain carbohydrate, phenols and proteins and are used to prevent

CC penetration of the fungal hyphae into the plant. The new M10 sequences

CC are used to generate transgenic plants resistant to fungal pathogens,

CC especially Erysiphe graminis (powdery mildew).

SQ Sequence 534 AA;

Query Match 98.4%; Score 2740; DB 20; Length 534;

Best Local Similarity 98.1%; Pred. No. 3, 2e-284;
Matches 524; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAEDYEPARTLPETPSMAVALFAVMIIIVSVLLEHALHKGHMFHRRKKNALAELEK 60
DB 1 MADDDYEPARTLPETPSMAVALFAVMIIIVSVLLEHALHKGHMFHRRKKNALAELEK 60
QY 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPSCLPGSVKSKYKDYCAKKGK 120
DB 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPSCLPGSVKSKYKDYCAKKGK 120
QY 121 SLMTSGSLHOLHIFIVLAVFHVTVSVIIMASRLKMKRTWKMETETASLEYOPANDPAR 180
DB 121 SLMTSGSLHOLHIFIVLAVFHVTVSVIIMASRLKMKRTWKMETETASLEYOPANDPAR 180
QY 181 FRFTHQTSFVKRHLGLSTPGIRWVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
DB 181 FRFTHQTSFVKRHLGLSTPGIRWVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
QY 241 FHKYIKRSMEDDFKVVVGISLPLMCVAILTLFLDIDIGITLTWISFIPVILLCVGTKLE 300
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DB 301 MIIMEMALEIODRASVIKGAPEVPSNKEFWFHRPDWVLFTHLTFPQNAFOQAHFVWTV 360
QY 361 ATPGLKCFPHMHIGLSIMKVVGLALQFLCSYTFPPLVALVTOMGSNNKRSIFDEQTAKA 420
DB 361 ATPGLKCFPHMHIGLSIMKVVGLALQFLCSYTFPPLVALVTOMGSNNKRSIFDEQTAKA 420
QY 421 LTNMNTAKKKKKVVDTDMLAQMIGDATPSRGTSPMPSRASPVHLHKGMRSDDPQS 480
DB 421 LTNMNTAKKKKKVVDTDMLAQMIGDATPSRGTSPMPSRASPVHLHKGMRSDDPQS 480
QY 481 APTSPRTMEARDMTPVVVAHPVHRLNPADRRSVSSALDADIPSADEFSSOG 534
DB 481 TPTSPRAMEARDMTPVVVAHPVHRLNPADRRSVSSALDADIPSADEFSSOG 534

RESULT 5

AAB31250
ID AAB31250 standard; Protein; 534 AA.

XX
AC AAB31250;

XX
DT 20-APR-2001 (first entry)

XX
DE Amino acid sequence of the wheat Mlo protein Trm101.

XX
KW wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KM powdery mildew; Mlo; cell wall apposition; transgenic plant.

XX
OS Triticum sp.

XX
PN MO200078799-A2.

XX
PD 28-DEC-2000.

XX
PF 16-JUN-2000; 2000MO-EP05576.

XX
PR 18-JUN-1999; 9905-0336112.

XX
PA (NOVS) NOVARTIS AG.

XX
PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.

XX
PI Salmeron JM, Weisio LJ, Strawn LJ, Kramer CM, Wang HX;

XX
PI Vernooij BT, Levin JZ, Helfetz PB, Patton DA, Que Q;

XX
DR WPI: 2001-112311/12.

XX
DR N-PSDB; AAF24583.

XX
PT Novel polynucleotide which encodes Mlo protein from wheat, useful for

PT producing fungal resistant plants, in particular wheat plant -
XX
PS Claim 12; Page 90-92; 128pp; English.

XX
CC The present sequence represents a Mlo protein. Mlo proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC Mlo proteins give resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews), in barley mutations at the Mlo
CC locus are responsible for a plant resistant phenotype. The mechanism
CC of Mlo resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding Mlo proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.

XX
SQ Sequence 534 AA;

Query Match 98.4%; Score 2740; DB 22; Length 534;
Best Local Similarity 98.1%; Pred. No. 3, 2e-284;
Matches 524; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAEDYEPARTLPETPSMAVALFAVMIIIVSVLLEHALHKGHMFHRRKKNALAELEK 60
DB 1 MADDDYEPARTLPETPSMAVALFAVMIIIVSVLLEHALHKGHMFHRRKKNALAELEK 60
QY 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPSCLPGSVKSKYKDYCAKKGK 120
DB 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPSCLPGSVKSKYKDYCAKKGK 120
QY 121 SLMTSGSLHOLHIFIVLAVFHVTVSVIIMASRLKMKRTWKMETETASLEYOPANDPAR 180
DB 121 SLMTSGSLHOLHIFIVLAVFHVTVSVIIMASRLKMKRTWKMETETASLEYOPANDPAR 180
QY 181 FRFTHQTSFVKRHLGLSTPGIRWVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
DB 181 FRFTHQTSFVKRHLGLSTPGIRWVAFFROFPRSVTKVDYLTLRAGFINAHLSHNSKFD 240
QY 241 FHKYIKRSMEDDFKVVVGISLPLMCVAILTLFLDIDIGITLTWISFIPVILLCVGTKLE 300
DB 241 FHKYIKRSMEDDFKVVVGISLPLMCVAILTLFLDIDIGITLTWISFIPVILLCVGTKLE 300
QY 301 MIIMEMALEIODRASVIKGAPEVPSNKEFWFHRPDWVLFTHLTFPQNAFOQAHFVWTV 360
DB 301 MIIMEMALEIODRASVIKGAPEVPSNKEFWFHRPDWVLFTHLTFPQNAFOQAHFVWTV 360
QY 361 ATPGLKCFPHMHIGLSIMKVVGLALQFLCSYTFPPLVALVTOMGSNNKRSIFDEQTAKA 420
DB 361 ATPGLKCFPHMHIGLSIMKVVGLALQFLCSYTFPPLVALVTOMGSNNKRSIFDEQTAKA 420
QY 421 LTNMNTAKKKKKVVDTDMLAQMIGDATPSRGTSPMPSRASPVHLHKGMRSDDPQS 480
DB 421 LTNMNTAKKKKKVVDTDMLAQMIGDATPSRGTSPMPSRASPVHLHKGMRSDDPQS 480
QY 481 APTSPRTMEARDMTPVVVAHPVHRLNPADRRSVSSALDADIPSADEFSSOG 534
DB 481 TPTSPRAMEARDMTPVVVAHPVHRLNPADRRSVSSALDADIPSADEFSSOG 534

RESULT 6

AA26968
ID AA26968 standard; Protein; 534 AA.

XX
AC AA26968;

XX
DT 21-DEC-1999 (first entry)

XX
DE wheat Mlo fungal resistance protein Trm103.

XX
KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KM papillae; contact site; callose; carbohydrate; phenol; transgenic plant;
XX Mlo; Erysiphe graminis; powdery mildew.

XX
OS Triticum sp.

Query Match	Best local similarity	Matches 513;	Conservative 11;	Mismatches 10;	Indels 0;	Gaps 0;
1	MADDYCPARTLPPTPSMAVALVAFVAMTVTVSVLLLEHAKHGWKHKRNKMALEALEK 60	96.3%;	Score 2680;	DB 20;	Length 534;	
1	MAKDDGTPPARKLPPTPSMAVALVAFVAMTVTVSVLLLEHAKHGWKHKRNKMALEALEK 60	96.1%;	Pred. No. 8.6e-278;			
61	IKAEMLVGFISLLIAVTDPIPGISGISKEAASIMRPSCLPQSGSVKSKYDKYCAKKGKV 120					
61	MKEMLVGFISLLIAVTDPIPGISGISOKAASIMRPSCKEYKSVKSKYDKYCAKKEKV 120					
121	SLASTGSLHQLIFEFVLAAPHNTYVVIIMALSRLLKMTKMKMETETASLEIYOFANDPAR 180					
121	ALMSTGSLHQLIFEFVLAAPHNTYVVIIMALSRLLKMTKMKMETETASLEIYOFANDPAR 180					
181	FRTHTQTSYVKNHGLASTPGIRIMVVAFFRPFQFSVTKVDYILIRAGFTINAHLSNKFKD 240					
181	FRTHTQTSYVKNHGLASTPGIRIMVVAFFRPFQFSVTKVDYILIRAGFTINAHLSNKFKD 240					
241	FHHYIKRSMEDDFKVVVGISLPLMCVAITLTLDDIGTIGTLMTISFPIVILLCYGTGLE 300					
241	FHHYIKRSMEDDFKVVVGISLPLMAVAITLTLDDIGTIGTLMTISFPIVILLCYGTGLE 300					
301	MIIMEALALIDQRBASVYIKGAVVYEPNSKFEFWRHDPDWLEFIIHLTFQNAFQMAHFVTV 360					
301	MIIMEALALIDQRBASVYIKGAVVYEPNSKFEFWRHDPDWLEFIIHLTFQNAFQMAHFVTV 360					
361	ATGGLKCKHMIIGISIMKVVYLGIALQFLCSYITPPLAYALTQWGSNMKRSIFEDBOTAKA 420					
361	ATGGLKCKHMIIGISIMKVVYLGIALQFLCSYITPPLAYALTQWGSNMKRSIFEDBOTAKA 420					
421	LITMNRMTAEKKKVVDDMLAQMIDGATIPSGTSPMSRRKSSVYHILHKGGRSDDPQS 480					
421	LITMNRMTAEKKKVVDDMLAQMIDGATIPSGTSPMSRRKSSVYHILHKGGRSDDPQS 480					
481	APTSPTMEADMTVVVAHVRHLNPADRRRSVSSALDADIPSDAFPSQSG 534					
481	APTSPTMEADMTVVVAHVRHLNPADRRRSVSSALDADIPSDAFPSQSG 534					

RESULT 7
AAB31252 ID AAB31252 standard; Protein; 534 AA.
XX
XX AAB31252;
XX
XX 20-APR-2001 (first entry)
XX
XX Amino acid sequence of the wheat Mlo protein TrmLo3.
XX
XX wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
XX powdery mildew; Mlo; cell wall apposition; transgenic plant.
XX
XX Triticum sp.
XX
XX WO200078799-A2.
XX
XX 28-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-EP05576.
XX
XX PF
XX 18-JUN-1999; 99US-0336112.
XX
XX PR
XX (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Salmeron JM, Weisio LJ, Stran LJ, Kramer CM, Wang HX;
XX Vernooij BJ, Levin JZ, Helfetz PB, Patton DA, Que Q;
XX WPI: 2001-11231/12.
XX
XX N-PSDB; AAF24585.
XX
XX Novel polynucleotide which encodes Mlo protein from wheat, useful for
XX producing fungal resistant plants, in particular wheat plant -
XX
XX Claim 12; Page 99-101; 128pp; English.
XX
XX The present sequence represents a Mlo protein. Mlo proteins given
XX resistance to fungal pathogens which infect living epidermal plant cells.
XX Mlo proteins give pathogens resistance to fungal pathogens, especially
XX Erysiphe graminis (powdery mildew). In barley, mutations at the Mlo
XX locus are responsible for a plant resistant phenotype. The mechanism
XX of Mlo resistance involves the formation of large cell wall appositions,
XX called papillae, at pathogen contact sites. Papillae mainly contain
XX callose, but also carbohydrates, phenols and proteins. Polynucleotides
XX encoding Mlo proteins are useful for making transgenic plants,
XX preferably wheat, which are resistant to fungal pathogens.
XX
XX Sequence 534 AA:
SQ
Query Match 96.3%; Score 2680; DB 22; Length 534;
Best Local Similarity 96.1%; Pred. No. 8.6e-278;
Matches 513; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
QY 1 MAEEYEPARLPETPSMAVAIVPAMTIIVSLLLEAHKLGHWHKHKNAALAELEK 60
DB 1 MAKDGGTPARLPETPSMAVAIVPAMTIIVSLLLEAHKLGHWHKHKNAALAELEK 60
QY 61 IKAELMIVGFISLLAVTODPISGICISERKASINRPSCLPPGSVSKSKIDYCKAKGKY 120
DB 61 MKAEIMIVGFISLLAVTODPISGICISOKASINRPSCKPPGSVSKSKIDYCKAKGKY 120
QY 121 SLNMGSLGOLHFIFFVLAVHHVYSYIIMASLRKMKMTKKMETASLEVOFANDPAR 180
DB 121 ALNMGSLGOLHFIFFVLAVHHVYSYIIMASLRKMKMTKKMETASLEVOFANDPAR 180
QY 181 FRFHQTSFVKRHLGLSTPGCIRNVAAFRRQFSRYTKVDYTLRLRGFINAHLSHNSKFD 240
DB 181 FRFHQTSFVKRHLGLSTPGCVNVAAFRRQFSRYTKVDYTLRLRGFINAHLSONSKFD 240
QY 241 FHKIKSMDDPFKVVVIGISLPLWCAVITLRLDIDIGTLTWISIPVIVLLCVGTRLE 300

Db 241 FHKIKRSMEDDFKVVYGISLPIMAVAITLFLDIDIGITLTWVSFPIILITLCVGTKE 300
 Qy 301 MIIMALEIQRASVYKCAPVPEPSNKEFFHPRDVLFFIHLTLFQNAFQMAHFVMTV 360
 Db 301 MIIMALEIQRASVYKCAPVPEPSNKEFFHPRDVLFFIHLTLFQNAFQMAHFVMTV 360
 Qy 361 ATPGLKCFHMHIGISIMKYVLALQFLCSYITPPLALVTOMSNKRSIFDEOTAKA 420
 Db 361 ATPGLKCFHMHIGISIMKYVLALQFLCSYITPPLALVTOMSNKRSIFDEOTAKA 420
 Qy 421 LTNMRTAKKKKRVDTMLAQMIGDAPTSRGTSMPSSRASSPVHLHKMGSRSDPOS 480
 Db 421 LTNMRTAKKKKRVDTMLAQMIGDAPTSRGTSMPSSRASSPVHLHKMGSRSDPOS 480
 Qy 481 APTSPRTMEARDMYPVYVAHPVHRLNPNADRRRSVSSALDADIPSADFSFSOG 534
 Db 481 APTSPRTMEARDMYPVYVAHPVHRLNPNADRRRSVSSALDADIPSADFSFSOG 534

RESULT 8

ID AAM59442 standard; Protein; 533 AA.
 AAM59442

AC AAM59442;
 DT 13-OCT-1998 (first entry)
 DE Hordeum vulgare MLO protein.
 KW MLO; mildew; pathogen; resistance.
 OS Hordeum vulgare.
 PN WO9804586-A2.
 PD 05-FEB-1998.
 PF 29-JUL-1997; 97MO-GB02046.
 PR 07-MAR-1997; 97GB-0004789.
 PR 29-JUL-1996; 96GB-0015879.
 PR 30-OCT-1996; 96GB-0022626.
 PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
 PI Buesches R, Panstruga R, SchulzeJelefert PMJ;
 DR WPI; 1998-159149/14.
 DR N-PSDB; AAV35022.
 PT New isolated MLO gene of barley - used to develop products for the
 PT production of transgenic plants which have increased pathogen
 PT resistance
 PS Claim 1; Fig 2; 150pp; English.
 CC The sequence is that encoded by the MLO gene, wild-type MLO
 CC exerts a negative regulatory function on a pathogen defence response,
 CC such that mutants exhibit a defence response in the absence of pathogen.
 CC Down-regulation or out-competition of MLO function may be used to
 CC stimulate a defence response in transgenic plants conferring increased
 CC pathogen resistance, especially resistance to powdery mildew or rust.
 CC The product can also be used for identifying compounds able to
 CC stimulate a defence response in a plant by interaction with
 CC encoded polypeptide.
 SQ Sequence 533 AA;

Query Match 87.4%; Score 2434; DB 19; Length 533;
 Best Local Similarity 89.2%; Pred. No. 2e-251;

Matches 471; Conservative 20; Mismatches 33; Indels 4; Gaps 3;

Qy 9 PARLPTPSMAVALVFAVMIIVSVLEHALHKGHMFHRRKRNALAELEKIKAEMLLV 68

Db 8 PARLPTPSMAVALVFAVMIIVSVLEHALHKGHMFHRRKRNALAELEKIKAEMLLV 67
 Qy 69 GFISLLAVYQDP-1SGCISEKASIMRPSL-PRGSYKSKYKYYCAKKGKSLMSTG 126
 Db 68 GFISLLIIVQDP1IKICISDADADVWPCCKGTGGRKPSKYVDY--CPGKVALMSTG 125
 Qy 127 SLHOLHFFIVLAVFHVYVSYVIALSLKMKRTKMKWETETSLSEYQANDPARFRTHQ 186
 Db 126 SLHOLHFFIVLAVFHVYVSYVIALSLKMKRTKMKWETETSLSEYQANDPARFRTHQ 186
 Qy 187 TSFVKRHLGLSTPGIRWVVAEFFROFESYKYVDYLTRAGFINAHLSHNSKDFHXYK 246
 Db 186 TSFVKRHLGLSTPGIRWVVAEFFROFESYKYVDYLTRAGFINAHLSONSKDFHXYK 245
 Qy 247 RSMEDDFKVVYGISLPIMAVAITLFLDIDIGITLTWVSFPIILITLCVGTKEMLTTEM 306
 Db 246 RSMEDDFKVVYGISLPIMAVAITLFLDIDIGITLTWVSFPIILITLCVGTKEMLTTEM 305
 Qy 307 ALEIQRASVYKCAPVPEPSNKEFFHPRDVLFFIHLTLFQNAFQMAHFVMTVATPGLK 366
 Db 306 ALEIQRASVYKCAPVPEPSNKEFFHPRDVLFFIHLTLFQNAFQMAHFVMTVATPGLK 365
 Qy 367 KCFHMHIGISIMKYVLALQFLCSYITPPLALVTOMSNKRSIFDEOTAKALTWMRN 426
 Db 366 KCFHMHIGISIMKYVLALQFLCSYITPPLALVTOMSNKRSIFDEOTAKALTWMRN 425
 Qy 427 TAKEKKKVRDTMLAQMIGDAPTSRGTSMPSSRASSPVHLHKMGSRSDPOSAPTSPR 486
 Db 426 TAKEKKKVRDTMLAQMIGDAPTSRGTSMPSSRASSPVHLHKMGSRSDPOSAPTSPR 485
 Qy 487 TMEARDMYPVYVAHPVHRLNPNADRRRSVSSALDADIPSADFSFSOG 534
 Db 486 TMEARDMYPVYVAHPVHRLNPNADRRRSVSSALDADIPSADFSFSOG 533

RESULT 9

ID AAB03401 standard; Protein; 533 AA.
 AAB03401

AC AAB03401;
 DT 27-OCT-2000 (first entry)
 DE Barley MLO protein sequence.
 KW Barley; MLO homologue; disease resistance.
 OS Hordeum vulgare.
 PN WO200036110-A2.
 PD 22-JUN-2000.
 PF 17-DEC-1999; 99WO-US30181.
 PR 18-DEC-1998; 98US-0112737.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Gahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
 DR WPI; 2000-431590/37.
 PT New polynucleotide encoding a MLO homologue polypeptide, useful for
 PT creating transgenic plants with altered levels of disease resistance -
 PS Example 2; Page 72-73; 79pp; English.
 CC The present sequence is the barley MLO sequence. MLO confers resistance
 CC to Erysiphe graminis f. sp. hordei upon the plant, and its inactivation
 CC leads to the priming of disease resistance even if the pathogen is not
 CC present. The protein, and its gene, can be used to create transgenic


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DE  Hordeum vulgare MLO protein homologue.
XX
XX  MLO; mildew; pathogen; resistance.
XX
OS  Hordeum vulgare.
XX
XX  WO9804586-A2.
XX
XX  05-FEB-1998.
XX
XX  29-JUL-1997; 97WO-GB02046.
XX
XX  07-MAR-1997; 97GB-0004789.
XX  29-JUL-1996; 96GB-0015879.
XX  30-OCT-1996; 96GB-0022626.
XX
XX  (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
XX  Bueschges R, Panstruga R, Schulzelefert PMJ;
XX
XX  WPI: 1998-159149/14.
XX  N-PSDB: AAV35030.
XX
XX  New isolated Mlo gene of barley - used to develop products for the
XX  production of transgenic plants which have increased pathogen
XX  resistance
XX
XX  Claim 8; Fig 14; 150pp; English.
XX
XX  The sequence is that encoded by a homologue of the MLO gene, wild-type
XX  MLO exerts a negative regulatory function on a pathogen defence response,
XX  such that mutants exhibit a defence response in the absence of pathogen.
XX  Down-regulation or out-competition of MLO function may be used to
XX  stimulate a defence response in transgenic plants conferring increased
XX  pathogen resistance, especially resistance to powdery mildew or rust.
XX  The product can also be used for identifying compounds able to
XX  stimulate a defence response in a plant by interaction with
XX  encoded polypeptide.
XX
XX  Sequence 544 AA:
XX
XX  Query Match 69.9%; Score 1946; DB 19; Length 544;
XX  Best Local Similarity 70.2%; Pred. No. 4e-199;
XX  Matches 384; Conservative 40; Mismatches 85; Indels 38; Gaps 3;
XX
XX  11 RTLPETPSMAVALVFAMVITVSYLLEHALHKLGHMFHRRKRNLALELRIKAEILMVG 70
XX  | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX  8 RELSDPTPMVAAYVCAVILVYSAMHHLKLGHHFHKRRKKALGELERKKADELIVGF 67
XX
XX  71 ISLLAVTQDPISGICISEKASIMRPSGLPPGSVSKSYKDY----- 113
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  68 ISLLAVTQDPISGICISEKASIMRPSGLPPGSVSKSYKDY----- 113
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  114 -----CAKKGKVSIMSTGSLHOLHIFIFVLAVFYVTVSYIIMASRLKMKRTKKRET 165
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  128 AARAGVDYCAKGGVVALMSGHSLHIFITVLAFFVLYSVTMTLSRLKMKQNNKWS 187
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  166 ETASLETOFANDPARFERHTQTSFVKRHLGLSSPGRVWVAEFRQFFSVTKVDYLTLR 225
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  188 ETASLETOFANDPSKRCRFTHTLVRRHLGLSTPGVWVAEFRQFFSVTKVDYLTLR 247
XX
XX  226 AGFINAHLSHNSKFDHFKHKKSMEDDFKVVVVGISLPLMCVATILTFLLIDIGLTMIS 285
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  248 OGFINAHLSOGNRPDDKTIKSLDEDDKVVVRSLSLKMVAALILFLDPDGIQLLMS 307
XX
XX  286 FLPVILLVCGTKLEIMIMEMALETOBRASVYKAPVPESENKFEWHRPDPVLFPHLT 345
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  308 VVPLVILLVWGTLEIMIMEMALETOBRASVYKAPVPESENKFEWHRPDPVLFPHLT 367
XX
XX  346 LFONAFOMAHFVTVATPGIKKCFMHHTGLSIMKVVLGLAOLFLGCTYTFEPLXYALYOMG 405
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX  368 LFONAFOMAHFVTVATPGIKKCFMHHTGLSIMKVVLGLAOLFLGCTYTFEPLXYALYOMG 427

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OY  406 SNMRSTFDEDTAKALTINRNRAKEKKKYVDJOMLMAOMIGDTPSRGTSMPSPASSPV 465
XX  | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  428 SHMRSTFDEDTAKALTINRNRAKEKKKYVDJOMLMAOMIGDTPSRGTSMPSPASSPV 479
XX
OY  466 HLHKGKGRSDDPQASPTSPRTMEARDMYPVVAHVHRLNAPDRRSVSSSLADADIP 525
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  480 HLHKGKGRSDDPQASPTSPRTMEARDMYPVVAHVHRLNAPDRRSVSSSLADADIP 534
XX
OY  526 SADFSFS 532
XX  | | | |
DB  535 GADGFS 541
XX
XX  RESULT 12
XX  AAW59444
XX  ID  AAW59444 standard; Protein; 536 AA.
XX
XX  AC  AAW59444;
XX
XX  DT  13-OCT-1998 (first entry)
XX
XX  DE  Oryza sativa MLO protein homologue.
XX
XX  KW  MLO; mildew; pathogen; resistance.
XX
XX  OS  Oryza sativa.
XX
XX  PN  WO9804586-A2.
XX
XX  PD  05-FEB-1998.
XX
XX  PF  29-JUL-1997; 97WO-GB02046.
XX
XX  PR  07-MAR-1997; 97GB-0004789.
XX  29-JUL-1996; 96GB-0015879.
XX  30-OCT-1996; 96GB-0022626.
XX
XX  (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
XX  Bueschges R, Panstruga R, Schulzelefert PMJ;
XX
XX  WPI: 1998-159149/14.
XX  N-PSDB: AAV35028.
XX
XX  New isolated Mlo gene of barley - used to develop products for the
XX  production of transgenic plants which have increased pathogen
XX  resistance
XX
XX  Claim 5; Fig 13; 150pp; English.
XX
XX  The sequence is that encoded by a homologue of the MLO gene, wild-type
XX  MLO exerts a negative regulatory function on a pathogen defence response,
XX  such that mutants exhibit a defence response in the absence of pathogen.
XX  Down-regulation or out-competition of MLO function may be used to
XX  stimulate a defence response in transgenic plants conferring increased
XX  pathogen resistance, especially resistance to powdery mildew or rust.
XX  The product can also be used for identifying compounds able to
XX  stimulate a defence response in a plant by interaction with
XX  encoded polypeptide.
XX
XX  Sequence 536 AA:
XX
XX  Query Match 62.4%; Score 1737.5; DB 19; Length 536;
XX  Best Local Similarity 65.8%; Pred. No. 8.5e-177;
XX  Matches 356; Conservative 57; Mismatches 95; Indels 33; Gaps 11;
XX
XX  10 ARTLPETPSMAVALVFAMVITVSYLLEHALHKLGHMFHRRKRNLALELRIKAEILMVG 69
XX  | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  8 SRELPEPTPMVAAYVCAVILVYSAMHHLKLGHHFHKRRKKALGELERKKADELIVGF 64
XX
XX  70 FISLLAVTQDPISGICISEKASIMRPSGLPPGSVSKSYKDY-----YCAK-K 117
XX  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  65 FISLLAVTQDPISGICISEKASIMRPSGLPPGSVSKSYKDY-----YCAK-K 124

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Qy	118	GVYSLMSTGSLHOLHITFVLANEHVTSVIMALSRLKRMKMKMETASLSEYOFAND	177
Db	125	GVKALMSAKSMHOLHITFVLANEHVTCILTMGLGRLKMKMKMESOTSLEYOFAD	184
Qy	178	PAHFRTQTSFVARNLIG--LSSTPGIRNVVAEPRFQFERSVTKVDYLLTLRAGFINAHLSHN	236
Db	185	PSHFRTQTSFVARNLIGSSSTPGIRNIVAEPFQFGSVTKVDYLLTMKGFINAHLSON	244
Qy	237	SKRDFKTKRKSMDDKPKVYVGSILPLMCVALTLFLPDIDIGITLMTLSPIPLVILLCVG	296
Db	245	SKRDFKTKRKSLDDPKVYVGSILPLMFVGLVLFDLHGLGTLTMTLSFPLILVLLVG	304
Qy	297	TKLEIMIMEMALIEIQDPAASYIGAPVPEBSKFEFHRPDMVLFTHLTLEFQNAFQNAHF	356
Db	305	TKLEIMIMEMAEIQDPAVYIGAPVPEBSKFEFHRPDMVLFTHLTLEFQNAFQNAHF	364
Qy	357	VWVAVATPGKACPFMHIGLSIMKVVVIGTALDPLCSYTFPFLYALVYOMGSMNKKSIIDEQ	416
Db	365	VWVAVATPGKACPFHENIMLSIVEIVIGISLQVCSYTFPFLYALVYOMGSMNKKRTIPEQ	424
Qy	417	TAAALTNRNRTAKKKKKVTRDTMLMAOMIGD--ATPSRGISPMPSRASSPYHLHLKKGGRS	475
Db	425	TKMALNNMKKAKMKKKRVKRDADFLQMSVDEATPA-----SSRSASEVHLL--QVTGRV	477
Qy	476	DDFQASPT--SPRTMEBARDMPVYVAHPEVHRL--NPADRRSSVSSALADIPSADFSF	531
Db	478	GRPSPTITVASPPAPEE--DMYEVPAALASRLDDPPDRRMWASSS--ADIADSDFSF	532
Qy	532	S 532	
Db	533	S 533	
RESULT 13			
ID	AAV26970	standard; Protein; 573 AA.	
XX	AAV26970;		
XX	21-DEC-1999	(first entry)	
XX	Arabidopsis thaliana	fungal resistance protein CIB10295.	
XX	Consensus:	resistance; fungus; pathogen; wheat; cell wall; apposition;	
KW	ppp1lla;	contact site; callose; carbohydrate; phenol; transgenic plant;	
KM	Mio; Erysiphe graminis;	powdery mildew.	
XX	Arabidopsis thaliana.		
OS	WO9947552-A2.		
XX	23-SEP-1999.		
XX	17-MAR-1999;	99MO-EP01779.	
XX	17-MAR-1998;	98US-0042763.	
PA	(NOVS) NOVARTIS AG.		
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
XX	Salmeron JM, Welslo LJ, Strawn LJ, Kramer CM;		
XX	WPI; 1999-571820/48.		
XX	DR N-PSDB; AA30413.		
XX	PT New proteins useful for generating transgenic plants resistant to		
XX	fungus infection -		
XX	Claim 3; page 78-81; 102pp; English.		
CC	This sequence represents the Arabidopsis thaliana fungal resistance protein CIB10295, which confers resistance to fungal pathogens by		

	CC	stimulating the formation of large cell wall appositions, designated papillae at the contact site with the fungal pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new MLo sequences are used to generate transgenic plants resistant to fungal pathogens, especially Erysiphe graminis (powdery mildew).	
xx	CC		
cc	XX		
S0	Sequence	573 AA:	
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Db	8		
Oy	71	ISLLAVTDDPSIGICISEKRAASIMPCGLPBGYSKYDY----- 112 :: :: :: :: :: :: :: :: :: :: :: :: :: :: ISLTLTGOTPISNICISOQAATSTMPCAAEAEEKGKKDAAGCKDGDGGCRGRLLLE 127	
Db	68		
Oy	113	-----YCAKKGVSLSMTSGSLHOLHIFFLVLANVPHTVSIIAMLSRL 155 :: :: :: :: :: :: :: :: :: :: :: :: :: :: LASVYIHRRSLATKGDKCAEKKAFVASYGIDHLNLFILVALVHVVCITYARGKI 187	
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Oy	156	KMRTRAKMETETASLEOFANDARRERFHOTSFPVKHNL--SSTGCIINVVAPPROFR 214 :: :: :: :: :: :: :: :: :: :: :: :: :: :: KMRTMSWEELKTLEYOASNDEPRFRFRADTSFGKRHLNFWSKTRVTLMIVCFEPDFG 247	
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Oy	273	LDDIGCTLTNSFLPIYLITCGTLEMIMENALETORASVINAGVAPPSPSKPMWF 332 :: :: :: :: :: :: :: :: :: :: :: :: :: :: TNSTGKASTLYLPFLPVLIIVGTKLLEVITLKDLARIQEKGDVNGARVYPDGDLFMF 367	
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DT	18-OCT-2000 (first entry)		
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 43648.		
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.		
KX			
OS	Arabidopsis thaliana.		
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PJ	EPI033405-AZ.		
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
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Query Match 45.9%; Score 1276.5; DB 21; Length 573;
 Best Local Similarity 48.8%; Pred. No. 2.4e-127;

Matches 251; Conservative 76; Mismatches 142; Indels 45; Gaps 4;

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QY 113 -----YCAKKGVSLSMSTGSLQHLITFVLAVFHYTVYIIMASRL 155
DB 128 LAESYIHRSLATKGYDCAKKGVA5VAYGIQHLITFVLAVHYVCIVYAFGKI 187
QY 156 KMRWKMKWETASLEYOAFNDPARFRFTHOTSPFKRHILG-SSTPGIRWVVAFFROFR 214
DB 188 KMRWKMSWEETKTIEYO5NDPERFRADT5FGKRHLNFMKSTRYTLMTIVCFRQFFG 247
QY 215 SVTKVDYITLRAGINAHLS--HNSKDFPHKIKYKSMEDDEKVVVGISLPLMCVALTLTF 272
DB 248 SVTKVDYIALRHGINAHNAPGNESRFRFKYIQRSLEKDFKTVVEISIVMEFVALFEL 307
QY 273 LDIDIGITLWISFIPVLVILLCVGTKEIMEMALEIODRASVIGAPVPSKKPFMF 332
DB 308 TNSYGLRSYLMPLRPIPLVYVILVGTKEIITKIGLQIOKRGDVAGCAVVPDGDLEWF 367
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AAB31254

ID AAB31254 standard; Protein; 573 AA.

AC AAB31254;

XX 20-APR-2001 (first entry)

XX Amino acid sequence of the Arabidopsis Mlo protein CIB10295.

XX Wheat: fungal resistance: fungal pathogen; Erysiphe graminis; papillae;

XX powdery mildew; Mlo; cell wall apposition; transgenic plant.

XX Arabidopsis thaliana.

XX WO200078799-A2.

XX 16-JUN-2000; 2000MO-BP05576.

XX 18-JUN-1999; 99US-0336112.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERN GRS MBH.

XX Salmeron JM, Welso LJ, Strawn LJ, Kramer CM, Wang HX;

XX Vernooij BT, Levin JZ, Helfetz PB, Patton DA, Que Q;

XX WPI: 2001-112311/12.

XX N-PSDB: AAF24587.

XX Novel polynucleotide which encodes Mlo protein from wheat, useful for

XX producing fungal resistant plants, in particular wheat plant

XX Claim 36; Page 108-110; 128pp: English.

XX The present sequence represents a Mlo protein. Mlo proteins given

XX resistance to fungal pathogens which infect living epidermal plant cells.

XX Mlo proteins give pathogens resistance to fungal pathogens, especially

XX Erysiphe graminis (powdery mildew). In barley, mutations at the Mlo

XX locus are responsible for a plant resistant pathotype. The mechanism

XX of Mlo resistance involves the formation of large cell wall appositions,

XX called papillae, at pathogen contact sites. Papillae mainly contain

XX callose, but also carbohydrates, phenols and proteins. Polynucleotides

XX encoding Mlo proteins are useful for making transgenic plants,

XX preferably wheat, which are resistant to fungal pathogens.

XX Sequence 573 AA:

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QY 11 RTLPETPSMAVALVFAVMITVSVLLEHALHLKLGHWFKRHKRNALAELEKIKALMYGF 70
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Tue Nov 19 14:16:01 2002

us-09-857-896a-32.rag

Page 12

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Page 4

[illegible]

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RESULT 7
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: Patent No. 6303332
: GENERAL INFORMATION:
: APPLICANT: Cahoon, Rebecca E.
: APPLICANT: Miao, Guo-Hua
: APPLICANT: Katalski, J. Antoni
: APPLICANT: Taramino, Grazzlana
: TITLE OF INVENTION: CORN DNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
: FILE REFERENCE: BB-1125
: CURRENT APPLICATION NUMBER: US/09/183,959
: CURRENT FILING DATE: 1998-11-02
: EARLIER APPLICATION NUMBER: 60/064,493
: EARLIER FILING DATE: No. 6303332member 5, 1997
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Microsoft Windows 95
: SEQ ID NO. 12
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: ORGANISM: Zea mays
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RESULT 8
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; Sequence 8, Application US/09183959

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? Patent No.6303332
? GENERAL INFORMATION:
? APPLICANT: Cahoon, Rebecca E.
? APPLICANT: Maao, Guo-Hua
? APPLICANT: Rafalski, J. Antoni
? APPLICANT: Tarantino, Grazia
? TITLE OF INVENTION: CORN DNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
? FILE REFERENCE: BB-1125
? CURRENT APPLICATION NUMBER: US/09/183,959
? CURRENT FILING DATE: 1998-11-02
? EARLIER APPLICATION NUMBER: 60/064,493
? EARLIER FILING DATE: No. 6303332ember 5, 1997
? NUMBER OF SEQ ID NOS: 20
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? SEQ ID NO: 8
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US-09-183-959-8

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GENERAL INFORMATION:
:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Miao, Guo-Hua
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
: TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
: FILE REFERENCE: BR-1125
:
CURRENT APPLICATION NUMBER: US/09/183,959
:
CURRENT FILING DATE: 1998-11-02
:
EARLIER APPLICATION NUMBER: 60/064,493
:
EARLIER FILING DATE: No. 6303332eember 5, 1997
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NUMBER OF SEQ. ID NOS.: 20

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; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 14
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; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-14
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; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 4
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-4
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Query Match
Best Local Similarity 50.0%; Score 187; DB 4; Length 80;
Matches 39; Conservative 11; Mismatches 26; Indels 0; Gaps 0;
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QY 232 HLSHNSKDFHXYKIRSMEDDFKVVGISLPLQCAVAILTLFDIDIGISTLWISFPLVI 291
      |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 HYPEKPDIDFHHKYMTRAVEYEFKRVGISWYLMLEVILFLLININGMHTYFWLAFLEPL 60
      |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 292 LIGVGTKEIMEMALE 309
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Db 61 LLIYGAKEHITITRLAQE 78
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RESULT 11
US-09-183-959-6
; Sequence 6, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
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; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
US-09-183-959-6
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Query Match
Best Local Similarity 46.2%; Score 127; DB 4; Length 52;
Matches 24; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
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QY 384 LALQFLCSYTFPLALVTQMSGHMKRSIFDEQAKALTNRNTAKKKRVR 435
      |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VVIXLCSYTFPLALVTQMSGCYKKEIFNEHVQGVLAGVAKVKKKGLR 52
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RESULT 12
US-08-808-793-4
; Sequence 4, Application US/08808793
; Patent No. 5858713
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,793
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,361
; FILING DATE: 24-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,649
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2104 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-793-4
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Query Match
Best Local Similarity 3.5%; Score 96.5; DB 2; Length 2104;
Matches 44; Conservative 34; Mismatches 89; Indels 31; Gaps 7;
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DB 382 LYOHVLAAG-PW-----HMLFFIYIFLG-----SFLVNLILAIYAMSY 421
QY 406 SNMKRSIDDEOTA--KALITMWRNTAKEK-KKYVRODTMLMAQMGIDATPSGTSMPMSRAS 462
DB 422 DELOKRAEEEAEEAIREAEAAAKAKLEERANVAQAQADADAAAALHPREMAK 481
QY 463 SPVH-----LLHKMGSRDDPOSAPTSPTMEARDMPYVVAHPVHRLNPADRRRSVS 516
DB 482 SPYSCISYELFVGEGKNDNNKEMKSTRSVESVSIVIQRPAPTPATKVKRVS 541
QY 517 SSALDADIPSADEFSFSG 534
DB 542 TTSL--SLPGSPFNLRG 557

RESULT 13
US-08-772-512A-4

; Sequence 4, Application US/08772512A
; Patent No. 6022705.
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Knipple, Douglas C.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
; TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772.512A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,618
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/601(CRPD-1657)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2104 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-772-512A-4

Query Match 3.5%; Score 96.5; DB 3; Length 2104;
Best Local Similarity 22.2%; Pred. No. 1;
Matches 44; Conservative 34; Mismatches 89; Indels 31; Gaps 7;

QY 346 LFONAFQMAHFVWTATPGKCFHMHIGLSIMKVVGLALQFLCSYTFPPYALVYQMG 405
DB 382 LYOHVLAAG-PW-----HMLFFIYIFLG-----SFLVNLILAIYAMSY 421
QY 406 SNMKRSIDDEOTA--KALITMWRNTAKEK-KKYVRODTMLMAQMGIDATPSGTSMPMSRAS 462

DB 422 DELOKRAEEEAEEAIREAEAAAKAKLEERANVAQAQADADAAAALHPREMAK 481
QY 463 SPVH-----LLHKMGSRDDPOSAPTSPTMEARDMPYVVAHPVHRLNPADRRRSVS 516
DB 482 SPYSCISYELFVGEGKNDNNKEMKSTRSVESVSIVIQRPAPTPATKVKRVS 541
QY 517 SSALDADIPSADEFSFSG 534
DB 542 TTSL--SLPGSPFNLRG 557

RESULT 14
US-08-808-793-3

; Sequence 3, Application US/08808793
; Patent No. 5858713
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808.793
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,361
; FILING DATE: 24-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,649
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2105 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-793-3

Query Match 3.5%; Score 96.5; DB 2; Length 2105;
Best Local Similarity 22.2%; Pred. No. 1;
Matches 44; Conservative 34; Mismatches 89; Indels 31; Gaps 7;

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DB 382 LYOHVLAAG-PW-----HMLFFIYIFLG-----SFLVNLILAIYAMSY 421
QY 406 SNMKRSIDDEOTA--KALITMWRNTAKEK-KKYVRODTMLMAQMGIDATPSGTSMPMSRAS 462
DB 422 DELOKRAEEEAEEAIREAEAAAKAKLEERANVAQAQADADAAAALHPREMAK 481

1
2
3

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OM protein - protein search, using sw model

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Perfect score: 2784
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Searched: 97044 seqs, 15060890 residues
Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/PCrUS_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	3.3	488	9 US-10-029-009-9	Sequence 9, Appl1
2	92	3.3	339	10 US-09-759-143-879	Sequence 879, App
3	92	3.3	339	10 US-09-780-669-879	Sequence 879, App
4	92	3.3	339	10 US-09-822-827-879	Sequence 879, App
5	92	3.3	505	9 US-10-029-009-21	Sequence 21, Appl1
6	90	3.2	267	10 US-09-747-835A-50	Sequence 50, Appl1
7	90	3.2	267	10 US-09-747-835A-51	Sequence 51, Appl1
8	88.5	3.2	363	10 US-09-864-761-42849	Sequence 42849, A
9	87.5	3.1	484	10 US-09-828-313-32	Sequence 32, Appl1
10	85.5	3.1	311	10 US-09-898-416-9	Sequence 9, Appl1
11	85.5	3.1	355	10 US-09-867-569-2	Sequence 32, Appl1
12	84	3.0	505	10 US-09-910-689-307	Sequence 307, App
13	84	3.0	505	12 US-10-010-742-307	Sequence 307, App
14	83.5	3.0	351	10 US-09-944-807-2	Sequence 2, Appl1
15	83.5	3.0	364	10 US-09-867-569-11	Sequence 11, Appl1
16	83	3.0	328	10 US-09-732-224-2	Sequence 2, Appl1
17	83	3.0	528	12 US-10-052-566-490	Sequence 490, App
18	83	3.0	543	10 US-09-732-224-5	Sequence 5, Appl1
19	83	3.0	584	12 US-10-094-214-2	Sequence 2, Appl1

20	82.5	3.0	451	10 US-09-925-637-22	Sequence 22, Appl1
21	82.5	3.0	811	10 US-09-815-242-11875	Sequence 11875, A
22	82	2.9	550	9 US-09-905-291A-227	Sequence 227, App
23	82	2.9	550	10 US-09-909-320-227	Sequence 227, App
24	82	2.9	550	10 US-09-909-088B-227	Sequence 227, App
25	82	2.9	550	12 US-10-052-586-46	Sequence 46, Appl1
26	81.5	2.9	416	10 US-09-927-616A-4	Sequence 4, Appl1
27	81.5	2.9	438	10 US-09-808-419-2	Sequence 2, Appl1
28	81	2.9	314	10 US-09-841-132-521	Sequence 521, App
29	81	2.9	364	10 US-09-775-879-15	Sequence 15, App
30	80.5	2.9	483	10 US-09-805-438A-6	Sequence 6, Appl1
31	80.5	2.9	494	9 US-09-981-947A-5	Sequence 5, Appl1
32	79.5	2.9	735	10 US-09-815-242-112089	Sequence 12089, A
33	79.5	2.9	855	10 US-09-828-307A-4	Sequence 4, Appl1
34	79.5	2.9	865	10 US-09-881-853-2	Sequence 2, Appl1
35	79.5	2.9	865	10 US-09-828-307A-2	Sequence 2, Appl1
36	79	2.8	1873	9 US-10-029-413A-22	Sequence 22, Appl1
37	78	2.8	1017	10 US-09-897-056-5	Sequence 5, Appl1
38	78	2.8	1018	10 US-09-815-242-5186	Sequence 5186, App
39	78	2.8	1210	10 US-09-922-217-692	Sequence 692, App
40	78	2.8	1210	10 US-09-833-263-692	Sequence 692, App
41	78	2.8	1548	10 US-09-922-217-1095	Sequence 1095, App
42	77.5	2.8	678	9 US-09-895-913A-4	Sequence 4, Appl1
43	77	2.8	2787	10 US-09-893-238-15	Sequence 15, Appl1
44	76.5	2.7	386	10 US-09-881-752A-74	Sequence 74, Appl1
45	76.5	2.7	425	10 US-09-815-242-12171	Sequence 12171, A

ALIGNMENTS

RESULT 1	US-10-029-009-9	Sequence 9, Application US/10029009
Patent No.	US20020164617A1	
GENERAL INFORMATION:		
APPLICANT:	Felisch, Jason S.	
APPLICANT:	Amis, David Allen	
APPLICANT:	Kalghatgi, Krishna	
APPLICANT:	Nash, Huw M.	
TITLE OF INVENTION:	Affinity Selection-Based Screening of Hydrophobic Proteins	
FILE REFERENCE:	111025.173 US2	
CURRENT APPLICATION NUMBER:	US/10/029, 009	
CURRENT FILING DATE:	2002-03-28	
PRIOR APPLICATION NUMBER:	US 60/258,970	
PRIOR FILING DATE:	2000-12-29	
NUMBER OF SEQ ID NOS:	34	
SOFTWARE:	FastSeq for Windows Version 4.0	
SEQ ID NO 9		
LENGTH:	488	
TYPE:	PRT	
ORGANISM:	Human	
US-10-029-009-9		
Query Match	3.3%; Score 93; DB 9; Length 488;	
Best Local Similarity	18.4%; Pred. No. 0.42;	
Matches	99; Conservative 73; Mismatches 171; Indels 196; Gaps 28;	
QY	17 PSMANA---LVFNAMITVSYLEHMLHKLGH---VF---HKRHKNA-----LAEALE 59	
DB	81 PSWRALMWSLAVGGVAVAV-----LGNLYIWIILAHKKRRVTVYFLVNLAFSDA 132	
QY	60 KIKAEIMLVGFISILLAVVODPIISGICISERKASIMRPSLPGSVSKYKDYCAKKGK 119	
DB	133 SAAAPNLTIVNLTVAL-----LHSEMYG-----HSEMYG----- 154	
QY	120 VSMKSTGSLHDLHFLFVAVFYVTVSYVIALSRMKMTKMTETASLEQYRANPDA 179	
DB	155 -----ANYCRFQNFEPITRAVFASTYSMAIALVDR-----YMAITDP- 190	
QY	180 RFRFTHQTSFYKRLHLSSTP---GIRNVVAF---PQFRFSYTKVDYTLTLAG---FI 229	
DB	191 -----LKPRLSATATKIVTIGIWIILAFLLAFQCLYSKTKV-----MPGRITLCFV 235	

Db 254 QSKIGIVSLGTHALL-----FAMNKKWI-----DIKQFVWYPTPEFMIAV----- 295
Qy 276 DGIGTLTWISFIFLVILL 293
Db 296 -----FLPIVVL 303

RESULT 4

US-09-822-827-879
; Sequence 879, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 879
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-879

Query Match 3.3%; Score 92; DB 10; Length 339;
Best Local Similarity 18.2%; Pred. No. 0.31;

Matches 58; Conservative 54; Mismatches 114; Indels 92; Gaps 13;

Qy 2 AEDYEP--ARTLEPTPSW-----AVALPFAVMIIVSVLLEHAKLIG---HWFKRHK 51
Db 52 ADEPDPSELQHTOELFPQWHLPIKIAAIASLFLYTLREVIRHPLATSHQYFYKIP 111
Qy 52 NALAEALERIKAEMLVGFISLLAVTQDPISGICISEKAASIMRPSLPQSVKSKYK- 110
Db 112 LVINKVLPWVSTTLALVYLPQVIAIVQHLNG-----TYKK 149
Qy 111 -----DYCAKKGKVSLSSTGSLHOLHIFFLVAVHYVSYI--IMASLKKRWKKW 163
Db 150 FPMHLDKMWLTKRQGLLS-----FFFAVLHAIYSLSYPMRSRYKKLMMAYO 198
Qy 164 ETEASLEQFANDPARPRFTHQTSFV---KRHLGSLSTPGI---RWVAFPRPFERS 215
Db 199 QVOQNKEDAMIEDVWRHEIYVSLGIVGAILLALLAVTSIPVSQSLTW-----REHYI 253
Qy 216 VTKVDYLTLRAGFIHAHLSHNSKDFEHKTKRSMEDFVVVGISLPLMCVAILTLFLDI 275
Db 254 QSKIGIVSLGTHALL-----FAMNKKWI-----DIKQFVWYPTPEFMIAV----- 295
Qy 276 DGIGTLTWISFIFLVILL 293
Db 296 -----FLPIVVL 303

RESULT 5

US-10-029-009-21
; Sequence 21, Application US/10029009
; Patent No. US20020164617A1
; GENERAL INFORMATION:
; APPLICANT: Felsch, Jason S.
; APPLICANT: Annis, David Allen
; APPLICANT: Kaignatgl, Kristina
; APPLICANT: Nash, How M.
; TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
; FILE REFERENCE: 111025.173 US2
; CURRENT FILING DATE: 2002-03-28
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21

; LENGTH: 505
; TYPE: PRT
; ORGANISM: Human
US-10-029-009-21

Query Match 3.3%; Score 92; DB 9; Length 505;
Best Local Similarity 18.3%; Pred. No. 0.55;
Matches 99; Conservative 73; Mismatches 171; Indels 198; Gaps 28;

Qy 17 PSMAYA---LVFAVMIIVSVLEHAKLIGH---WF---HKRHKNA-----LAELE 59
Db 97 PSMRIALMSLAVGVAAVAV-----LGNLYIYIITIAHKKRRVTVYFLVNLAFSDA 148
Qy 60 KIKAEMLVGFISLLAVTQDPISGICISEKAASIMRPSLPQSVKSKYKDYCAKKGK 119
Db 149 SMAENLTIVNEFYAL-----HSEWYFG--- 170
Qy 120 VSLMSTGSLHOLHIFFLVAVHYVSYIIMASLKKRWKKWETASLEQFANDPA 179
Db 171 -----ANYCRPQNEFFITAVFASYSMTALVDR-----YMAIIDP- 206
Qy 180 RERTHQTSFYKRLHGLSTP---GIRVVAF---FROFPRSVTKVDYLTLRAG---FI 229
Db 207 -----LKPRLSTARKIYIGSIWILAFLLAFPOCLYSKTKV-----MPGRTLGFV 251
Qy 230 NAHLSHNSKDFEHKTKRSMEDFVKVVGISLPLMCVAILTLFLDIDGIGTLTWISFPL 289
Db 252 QMPESPCKQHTYH-----IIVIIIVYCPFLIMGITYTIVIGILMGGEIP- 296
Qy 290 VILLGVTKLEMIIMEMALEIODRASVIRKGAHVPEPSNKFVW---FHRPDMVLEFHLTLF 347
Db 297 -----GDTCD---KYHEQLKAKRKVVVMIIYVFAICWLPYH-----IYFILTYIY 341
Qy 348 Q-----NAFOAHFVW-----TVAFGKCKCFHMHIGLSIMKVVGLALOPFCSYIT 394
Db 342 QQLNWKRYIQOYVLASF-WLAMSSTYNYNIICLNKFRAGFR-----ARRW-CPLIK 394
Qy 395 PPLY---ALVYQMSNKKRSIDEDQAKALT-----NMRNTAKEKKYRQDTMLMAQNI 445
Db 395 VSSYDELKTKTRPHPRQSSMYTVYRMSMSMVFEDPADVATRSSKKR----- 444
Qy 446 GDATP-----SRGTSPPMPSRASSPVILLKKGGRSDPOSAPTS-----RTMEAR 492
Db 445 ---ATPRDPSFNGCSRNRKSASATSSFISPTYSDEISQPELAPEDPADAKHKLQDLR 502
Qy 493 D 493
Db 503 N 503

RESULT 6

US-09-747-835A-50
; Sequence 50, Application US/09747835A
; Patent No. US20020146692A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhang, Jie
; APPLICANT: Ken, Felyan
; APPLICANT: Asundi, Vinod
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: HYS-37CIP
; CURRENT FILING DATE: 2002-03-08
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/729,739
; PRIOR FILING DATE: 2000-08-31

;; PRIOR APPLICATION NUMBER: US 09/620,312
;; PRIOR FILING DATE: 2000-07-19
;; PRIOR APPLICATION NUMBER: US 09/598,042
;; PRIOR FILING DATE: 2000-06-20
;; PRIOR APPLICATION NUMBER: US 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: US 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 50
;; LENGTH: 267
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-747-835A-50

Query Match 3.2%; Score 90; DB 10; Length 267;
Best Local Similarity 18.3%; Pred. No. 0.35;
Matches 55; Conservative 50; Mismatches 106; Indels 90; Gaps 12;

QY 17 PSW-----AVALFVAVMIIVSVLLEHAKLKG---HMFHKKRNALAELEKIKAEMLV 68
DB 3 PQWHLPIKIAIILASITFLYLLREVIHPLATSHOOYFYKIPILVINKVLPMSITLLAL 62
QY 69 GFISLLAVTQDPISGICISEKAASIMRPSLPPGSVSKYK-----DYCAKKGKVS 122
DB 63 VYLPGVIAIAIVQIHNG-----TKYKFPFHMIDKMKMLTRKQFGL 100
QY 123 MSTGSLHQLHIFVLAIVHYTVSVI--IMALSRLKMTKMTKMETETASLEVOFANDPAR 180
DB 101 LS-----FFAVLHAIVLSLSPMRRSRYRKLNMAYQVOQNKEDAMTEHDVWR 149
QY 181 FRFHQTSFV-----KRHLGSLSTPGI---RWVAFPROFPRSVTKVDYLLRAGFTNAH 232
DB 150 MEIYVSLGIYGLAIIALLAVTSIPSVDSLTW-----REFHYIOSKIGIYSLIGTIAL 204
QY 233 LSHNSKFEFHKYIKRSMEDDFKVVVGISLPLMCVAIITFLDIDIGITLTWISFIPVYL 292
DB 205 I-----FANWKMT-----DIKQFVWYTPPTFMIAV-----FLPIVYL 236
QY 293 L 293
DB 237 I 237

RESULT 7
US-09-747-835A-51
; Sequence 51, Application US/09/47835A
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Asundi, Vinod
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
; FILE REFERENCE: HYS-37CIP
; CURRENT APPLICATION NUMBER: US/09/747,835A
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/729,739
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/552,317

;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: US 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 51
;; LENGTH: 267
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-747-835A-51

Query Match 3.2%; Score 90; DB 10; Length 267;
Best Local Similarity 18.3%; Pred. No. 0.35;
Matches 55; Conservative 50; Mismatches 106; Indels 90; Gaps 12;

QY 17 PSW-----AVALFVAVMIIVSVLLEHAKLKG---HMFHKKRNALAELEKIKAEMLV 68
DB 3 PQWHLPIKIAIILASITFLYLLREVIHPLATSHOOYFYKIPILVINKVLPMSITLLAL 62
QY 69 GFISLLAVTQDPISGICISEKAASIMRPSLPPGSVSKYK-----DYCAKKGKVS 122
DB 63 VYLPGVIAIAIVQIHNG-----TKYKFPFHMIDKMKMLTRKQFGL 100
QY 123 MSTGSLHQLHIFVLAIVHYTVSVI--IMALSRLKMTKMTKMETETASLEVOFANDPAR 180
DB 101 LS-----FFAVLHAIVLSLSPMRRSRYRKLNMAYQVOQNKEDAMTEHDVWR 149
QY 181 FRFHQTSFV-----KRHLGSLSTPGI---RWVAFPROFPRSVTKVDYLLRAGFTNAH 232
DB 150 MEIYVSLGIYGLAIIALLAVTSIPSVDSLTW-----REFHYIOSKIGIYSLIGTIAL 204
QY 233 LSHNSKFEFHKYIKRSMEDDFKVVVGISLPLMCVAIITFLDIDIGITLTWISFIPVYL 292
DB 205 I-----FANWKMT-----DIKQFVWYTPPTFMIAV-----FLPIVYL 236
QY 293 L 293
DB 237 I 237

RESULT 8
US-09-864-761-42849
; Sequence 42849, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

RESULT 9
US-09-828-313-32
: Sequence 32, Application US/09828313
: Patent No. US20020059662A1
: GENERAL INFORMATION:
: APPLICANT: COSTA e SILVA, OSMALDO DA
: APPLICANT: BOHNETT, HANS J.

```

RESULT 10
US-09-898-416-9
; Sequence 9, Application US/09898416
; Patent No. US20020076759A1
; GENERAL INFORMATION:
; APPLICANT: Duclac, Catherine
; APPLICANT: Axel, Richard
; TITLE OF INVENTION: Cloning Of Vertebrate Pheromone Receptors And Uses
; TITLE OF INVENTION: Theriof
; FILE REFERENCE: 0575/48557A/JPW/ADM
; CURRENT APPLICATION NUMBER: US/09/898,416
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 08/731,745
; PRIOR FILING DATE: 1996-10-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 311

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TYPE: PRT
ORGANISM: Rattus sp.
US-09-898-416-9

Query Match 3.1%; Score 85.5; DB 10; Length 311;
Best Local Similarity 21.6%; Pred. No. 1.2;
Matches 64; Conservative 54; Mismatches 105; Indels 73; Gaps 16;

QY 233 LSHNSKDFHKKYKRSMEDEDFVYVIGISLPMCAVL-TLFLDIDG-----IGTLT 262
DB 2 MNKNSRL-----HIDSNIRNTEFTEIGVANSLSLLEFNFEKFIHQSRSLTDLPIGLS 57
QY 283 WISPIPLVILLCVGKTL-----EMIME-----MALEIODRASVYKAGAPVE 324
DB 58 LTNLMMLIMACIATDIFISCRWDIDICKSLTYLTKFRGSLSTTCCLSLVLA-ATLS 116
QY 325 PSNKF--WFHPRDWLFPFIHLL-FQAFQMAHFVWT-VAPPGKCKCFHMHIGLSIMKY 380
DB 117 PRSSCLAKYKHKPPHIFCAMLFSLVLYMFSSHLSTIATPNTLTDNFIVSQS----- 172
QY 381 VGLALQFLCSYTFPLVALVTQMGSNK-RSIFDEQAKALTMNRMTA-----KEKK 432
DB 173 -----CSIL--PMSYLMQSMFSTLLAIRNF-LISLIVLSTWYVWALLCRHKKOTR 220
QY 433 KVRDPMALMOMIGDAPPSRGTSPMPSRASSPVHLHKKGREDPOSAFPTSPRTM 488
DB 221 HLQDTSL-----SRKASP-EQATRSILMLSLFGLMSIFDSIASCSRTM 264

RESULT 11
US-09-867-569-2
Sequence 2, Application US/09867569
Patent No. US2001003650A1
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: C5a Receptor
FILE REFERENCE: PFI30DICI
CURRENT APPLICATION NUMBER: US/09/867, 569
CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/082,529
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: 08/458,970
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/09234
PRIOR FILING DATE: 1994-08-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 355
TYPE: PRT
ORGANISM: homo sapiens
US-09-867-569-2

Query Match 3.1%; Score 85.5; DB 10; Length 355;
Best Local Similarity 19.3%; Pred. No. 1.4; Indels 179; Gaps 24;
Matches 81; Conservative 55; Mismatches 104; Indels 179; Gaps 24;

QY 111 DYCAKKGKVSLSMSTGSLHQLHIFFLA-----VHVTYSVITMALSRLKMRWK 161
DB 20 DYSLSESDLEKQVQGVHWSLVLYCLAFLGIPGKCLYHLVGV-----QVEDSHT 73
QY 162 KWETETASLEQF-----ANDPARPFTQTSFVVRHGL 196
DB 74 LMFNLALADIFLLFLPLXYISVAMNFMPPGWTLCRANS-----FTQQLM----- 121
QY 197 SSTPGIRWYVAFRQFFRSYTKVD-YLTLRAGFINAHLSHNSKDFEHKXIKRSMEDDKV 255
DB 122 -----FASVEFLVYISLDHYHL-----IHPVLSHR-----HRTLKNSL-----I 156
QY 256 VVGISLPLMCAVL-----TLFL-----DIDGI--GTLTWISFIP 288
DB 157 VI---IFIMVLASLIGGPAIYFRDIVERNNHTLWYNNFQKHDPDLTKRHVHVLWVKFI- 212

QY 289 LVILLCVGKTEKIME-----MALEIODRASVYKAGAPVEPSNKFPM----- 331
DB 213 -----IGLFPPLMMSIRYLCLIFVKKRSLLI-----SRHFTLIVVYVAFVW 258
QY 332 ---FHRPDMVLEFI-HLLFQNAFQMAHFVWTVAAPGKCKCFHMHIGLSIMKYGLALQ 387
DB 259 WMPYH-----LFSIGELTIHNSY--SHHVMOAGIP-----LSTGTLA 293
QY 388 FLCSYTFPLVALVTQMGSNKRSIFDEQAKAL--TNMR-----NTAKKKVRODML 440
DB 294 FLNSCLNPLIYLV-----SKRQARPRSSVALIILTYIMEVSCSGIVSBDLRNSEIKNL 348

RESULT 12
US-09-910-689-307
Sequence 307, Application US/09910689
Patent No. US20020081609A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Uiang, Tuglu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.491C6
CURRENT APPLICATION NUMBER: US/09/910,689
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 307
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-689-307

Query Match 3.0%; Score 84; DB 10; Length 505;
Best Local Similarity 18.7%; Pred. No. 3.4; Indels 208; Gaps 31;
Matches 98; Conservative 74; Mismatches 143; Indels 208; Gaps 31;

QY 17 PSM-----AVALVFAMIVISVLL-----BHALKL-----GHMF--HKR--- 49
DB 3 PSMLOEIMAHNPELILLILCSLLLFQYIRLYORRRMIRALHLPAPAMFYGHKEFYR 62
QY 50 -----HKNALAELEKIKAEML-VGFSILLAVTQDPTSGICISEKASIMRCSLP 101
DB 63 VKEEFYHK-----LMEYPCAVPLWVGPTMFEV-HDP-----DYAKTLKRDP 108
QY 102 PGSVKSKYKDYCAKKGKVSLSMSTGSLHQLH-----IFFLAVFHVTYSVITMALS- 153
DB 109 KSAVSHKILIESVWG-RGLVTL--DGSWKHKRQIVAPGFNISILKIF-----ITMSESV 160
QY 154 RLKMRWKKWETETASLE-VQFA-----NDPARPFTQTSFVVRHGLSGSTGIMVYA 207
DB 161 RMPLNKMEERIAQNSRLLEFQVHSVSLMTLDSIMKCAFSHOGS-----IQDST----- 207
QY 208 FFRQFFRSYTKVDYLTLRAGFINAHLSHN-----SKF--DFHKYIKRSMED- 251
DB 208 -LDSYLKAVFNLSKISNR--MNNFLHNDLVKFSOGQIFSRFNOELHQFTEKVIDOR 264
QY 252 -----DFKVYV-----GTS 260
DB 265 KESLKDKLKODTQKRWDIDILLSAKSENTKQSEADLQAEVKTMTMFGHDTTSSAIS 324
QY 261 LPLMCAV-----LTLFLDIDGIGLTV--ISFIPLVILLCVGKTEKIMT----- 302
DB 325 WILYCLAKYRHHQRCRDEIRELLGDGSSI--TWETHLSQPHY-TWCIKRECLRLVAPVY 380
QY 303 ---IMEALEIODRASVYKAGAPV-----VESNKFPM-----FHRPDMVLEFIIH 343

Db 381 NISRLDKPITPPDGRSLPAGITVFVIMALHNNHPTWEDQOVNPLRFSR----- 431
QY 344 LTLFONAFOMAHFWVTATPGLKCFHMHIGLSIMKVVIGLAL 386
Db 432 ----ENSEKHIPYAFIPFSAGLRNCIGOHFAITIECKVAVALTL 470

RESULT 13

US-10-010-742-307
Sequence 307, Application US/10010742
Patent No. US20020146727A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bennington, Angela Ann
APPLICANT: Zehentner, Barbara
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.491C7
CURRENT APPLICATION NUMBER: US/10/010,742
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 307
SOFTWARE: fastseq for windows version 4.0
SEQ ID NO 307
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-10-010-742-307

Query Match 3.0%; Score 84; DB 12; Length 505;
Best Local Similarity 18.7%; Pred. No. 3.4;
Matches 98; Conservative 74; Mismatches 143; Indels 208; Gaps 31;

QY 17 PSM-----AVALPAMVMIIVSVL-----EHALHKL---GHWF---HRR--- 49
Db 3 PSMLOELMAHPFLILLICMSLLLFQVIRLYQRRMMIRALHLPAPPAWFGHKEFP 62
QY 50 -----HKNALAEKIKAEIML-VGPISLLAVYODPISGICISERKASIMPCSLP 101
Db 63 VKEFEVYHK-----LMKIPCAVPLWVGFTWFEFSV-HDP-----DYAKILLKRODP 108
QY 102 PGSVKSKYKDYCAKKGKSLMSTGSLHQLH-----IFEVLAHVYVSYIIMALS- 153
Db 109 KSAVSHKILLESWG-RGLVYL--DGSKKMKHROIVKPGFNISILKIP-----ITMSESV 160
QY 154 RLKMRWKMKMETETASLE-YQFA-----NDARFETTHQTSFYKRIHGLSSPIGIRWYVA 207
Db 161 RMLNKKMEERIAONSRLLEFQHSLSMTLDSIMKCAFHSQGS-----IQDST----- 207
QY 208 FFROPFSVTKVDYLLIRAGFINAHLSN-----SKF--DFHKYIKRSMED- 251
Db 208 -LDYLAHAVNLKISNOR--NMNPLHNDLVFRSSOGOFSEKFNQELHOFTEKVIDR 264
QY 252 -----DPKVVY-----GIS 260
Db 265 KESLKDRLKQDTQKRMPDLILLSAKSENTKDFSEADQAEVKTFPMRAGHDTTSSAIS 324
QY 261 LPLMCVA-----LTLFLDIDIGITLW--ISFPLVILLCVGTKLEMI----- 302
Db 325 WILCYLAKPYEHOQRDEIRLELDGSSI---TWELHLSQMPYT-TMCIKECLRLYAPV 380
QY 303 ----IMEALEIODRASVIKAPV-----VPSNKKPFM-----PHRDWLFFTH 343
Db 381 NISRLDKPITPPDGRSLPAGITVFVIMALHNNHPTWEDQOVNPLRFSR----- 431

QY 344 LTLFONAFOMAHFWVTATPGLKCFHMHIGLSIMKVVIGLAL 386
Db 432 ----ENSEKHIPYAFIPFSAGLRNCIGOHFAITIECKVAVALTL 470

RESULT 14

US-09-944-807-2
Sequence 2, Application US/09944807
Patent No. US200119494A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: Influence inflammatory conditions of chronic
FILE REFERENCE: 082.00p
CURRENT APPLICATION NUMBER: US/09/944,807
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: UK 0021484.1
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 351
TYPE: PRT
ORGANISM: Homo sapiens
US-09-944-807-2

Query Match 3.0%; Score 83.5; DB 10; Length 351;
Best Local Similarity 22.5%; Pred. No. 2.2;
Matches 63; Conservative 41; Mismatches 95; Indels 81; Gaps 17;

QY 236 NSKRFPHYIKRSMEDDFVYVIGSILPMCAVILTLFLDIDIGITLWISFPL----YIL 292
Db 4 NESTPLMEYEVSYESAGTYLRI-LPLVYLVG-VTVYLGVLGVLWVAGFRMTRTVTT 61
QY 293 LC-----VGRKLEIMEMALEIODRASVYKAGAPVPSNK--FFWFHPPDWLF 340
Db 62 ICYLNIALADFSFTATLPLIVSNM-----GEKWFPGMF-----LCK 99
QY 341 FHTLPLONAFOMAHFWVTATPGLKCF-----HMHIGLSIMKVVIG---LALQ 387
Db 100 LIHIVYDINLFGSVFLIGIA---LDRCICYLHPWAQNHKRVSLA-KKVLVGFMIALL- 154
QY 388 FLCVITFPYLALVTOM-----GSNNKRSIFDEQATAKALTNNWNTAKKKKRVDTMLMAQ 443
Db 155 ----VTLPLVFLFLTYTIPNG-----DYCTFNFAVSGGTPEERLKAIT-MLTAR 201
QY 444 ----MIGATPSRGTSPPMSRASPVYLLHKGGRSDP 478
Db 202 GIIRFVIGFSLPMSIATVACVGLIAAKTH--KKGMKISSRP 239

RESULT 15

US-09-867-569-11
Sequence 11, Application US/09867569
Patent No. US2001003650A1
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Csa Receptor
FILE REFERENCE: PFI30D1C1
CURRENT APPLICATION NUMBER: US/09/867,569
CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/082,529
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: 08/458,970
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/09234
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 364
TYPE: PRT

; ORGANISM: mus musculus
us-09-867-569-11

Query Match 3.0%; Score 83.5; DB 10; Length 364;
Best Local Similarity 21.5%; Pred. No. 2.4;
Matches 53; Conservative 40; Mismatches 85; Indels 69; Gaps 14;

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OY 256 VVGISLPKCVAILFLFDIDIGITLWISFIPVLV-LCVGTKLEMIMEMALEIODRA 314
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 49 VLGGLVIMVAGFRMKH-----TVTTISLNLALADPCFTSTLPFYI-----A 91
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 315 SVIKGA--PYVEPSNKEFWFHRPDMVLEFIHLTFQNAFQA-----HFVWTV 361
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 92 SMVWGCHWP-----FGWF-MCKFIYTVIDINLFGSVFLIALIALDRICICVLPVMA-- 141
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 362 TPGLAKCFHHHIGLSIMKVVGLALQFLGSY-ITPPLVXALVT-----OMGSNMKRSTFDE 415
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 142 -----QNHRTVSLAKV--ITVPWICAFLLPLFVIIRLTTPVNSRLGPGKTACTFD- 190
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 416 QTAKALTNMNTAKKKKKVDTDM---LMAQMIQDATPSRGTSPPSRASSPVHLLHG 471
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 191 ----FSPMTKDPVEKKKVAVMMLTVRGIIIRFIIGFSTPMSIVAICYGILTTKIH--RQG 243
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 472 MGRSDDP 478
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 244 LIKSSRP 250
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Search completed: November 18, 2002, 15:47:00
Job time : 36 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 15:40:28 / Search time 2879 Seconds

(without alignments)
5398.020 Million cell updates/sec

Title: US-09-857-896a-32

Perfect score: 2784 1.MEDIEYPPARTLPEPESMA.....YSSSALDADIPADFSPSG 534

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
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2: gb_hgt:*
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5: gb_ov:*
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17: em_hum:*
18: em_in:*
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22: em_ov:*
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30: em_hgt_hum:*
31: em_hgt_inv:*
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38: em_sy:*
39: em_hgt_hum:*
40: em_hgt_mus:*
41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2777	99.7	1693	6 AX063296	AX063296 Sequence
2	2740	98.4	1868	6 AX063294	AX063294 Sequence
3	2736	98.3	1730	8 AF361932	AF361932 Trilicium
4	2718	97.6	1721	8 AF384145	AF384145 Trilicium
5	2681	96.3	1819	8 AF384144	AF384144 Trilicium
6	2680	96.3	1886	6 AX063298	AX063298 Sequence
7	2434	87.4	1602	6 A92828	A92828 Sequence
8	2434	87.4	1917	6 A92833	A92833 Sequence
9	2434	87.4	1917	6 A92833	A92833 Sequence
10	2205	79.2	1399	8 AF361933	AF361933 Trilicium
11	2032.5	73.0	1740	8 AF384030	AF384030 Oryza sat
12	1972.5	71.0	59748	8 HVCH4H	HVCH4H
13	1860	70.4	1635	6 A92838	A92838 Sequence
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15	1850	66.5	1872	8 AY029312	AY029312 Zea mays
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RESULT 1

ALIGNMENTS

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LOCUS AX063296 Sequence 5 from Patent W0078799.
DEFINITION AX063296
ACCESSION AX063296
VERSION AX063296.1 GI:12541086
KEYWORDS
SOURCE
ORGANISM
Triticum sp.
Triticum sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
REFERENCE
1 (bases 1 to 1693)
Salmeron, J. M., Wells, L. J., Strawn, L. J., Kramer, C. M., Wang, H. X.,
Vernooij, B. T., Levin, J. Z., Helfetz, P. B., Patton, D. A. and Que, Q.,
M10-genes controlling diseases
Patent: WO 0078799-A 5 28-DEC-2000;
Novartis AG (CH)
FEATURES
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QY	501	HisProValHisArgLeuAsnProAlaAspArgArgSerSerSerSerAlaLeu	520
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DEFINITION	Sequence 3 from Patent WO07/8799.		
ACCESSION	AX063294		
VERSION	AX063294.1	GI:12541084	
KEYWORDS			
SOURCE			
ORGANISM	Triticum sp.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticaceae; Triticum.		
AUTHORS	1 (bases 1 to 1868)		
TITLE	Salmon, J.M., Weislo, L.J., Straw, L.J., Kramer, C.M., Wang, H. X., Vernon, J.B.T., Levin, J.Z., Helfetz, P.B., Patton, D.A. and Que, Q.		
JOURNAL	MtO-genes controlling diseases Patent: WO 0078799-A 3 28-DEC-2000; Novartis AG (CH)		
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LOCUS Trilicium aestivum seven transmembrane-spanning protein (MLO2) mRNA,
DEFINITION complete cds.
ACCESSION AF361932
VERSION AF361932.1 GI:15290588
KEYWORDS
SOURCE
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Trilicium aestivum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triliceae; Trilicium.
REFERENCE
AUTHORS Devoto, A., Hartmann, A., Piffanelli, P., Elliott, C., Simmons, C.,
Taramino, G., Goh, C.-S., Schulze-Lefert, P. and Panstruga, R.
TITLE Co-Evolution among intracellular domains and the C-terminus of the
seven-transmembrane MLO protein is suggested by a detailed
computational analysis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1730)
AUTHORS Elliott, C.E. and Schulze-Lefert, P.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2001) The Sainsbury Laboratory, John Innes
Center, Colney Lane, Norwich NR4 7UH, UK
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 AF384145 AF384145
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 ORGANISM Triticum aestivum
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 REFERENCE
 Yu, L., Niu, J.-S., Ma, Z.-O., Chen, P.-D. and Liu, D.-J.
 1 (bases 1 to 1721)
 Cloning, characterization analysis and expression of MLO1 gene from

JOURNAL wheat
 REFERENCE 2 (bases 1 to 1721)
 AUTHORS Yu, L., Niu, J.-S., Ma, Z.-O., Chen, P.-D. and Liu, D.-J.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAY-2001) Key Laboratory of Crop Cytogenetics,
 Nanjing Agricultural University, Nanjing, Jiangsu, China
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DEFINITION Trilicium aestivum MLO protein mRNA, complete cds.
ACCESSION AF384144
VERSION AF384144.1 GI:14334166
KEYWORDS
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ORGANISM
Trilicium aestivum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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1 (bases 1 to 1819)
REFERENCE
YU, L., NIU, J.-S., MA, Z.-Q., CHEN, P.-D. and LIU, D.-J.,
Cloning, location and expression of MLO gene from wheat
unpublished
2 (bases 1 to 1819)
AUTHORS
YU, L., NIU, J.-S., MA, Z.-Q., CHEN, P.-D. and LIU, D.-J.
TITLE
Direct Submision
JOURNAL
Submitted (23-MAY-2001) Key Laboratory of Crop Cytogenetics,
Nanjing Agricultural University, Nanjing, Jiangsu, China
LOCATION/Qualifiers
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AX063298.1 GI:12541088
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 1886)
AUTHORS
Salmeron J.M., Weislo J.J., Strawn L.J., Kramer C.M., Wang H.X.,
Vernooij B.T., Levin J.Z., Helfetz P.B., Patton D.A. and Que Q.
TITLE
Mlo-genes controlling diseases
JOURNAL
Patent: W0 0078799-A 7 28-DEC-2000;
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US-09-857-896a-32 (1-534) x AX063298 (1-1886)

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Oy	281	LeuThrTrpIleSerPheIleProLeuValIleLeuLeuCysValAlaGlyThrLysLeuGlu	300
Db	1038	CTCAGCTGGGTTCCTTCATCCCTCATCATCTCTTGTGTGGTGGAAACAACATCTAG	1097
Oy	301	MetIleIleMetGluMetAlaLeuGluIleGluAspArgAlaSerValIleLysGlyAla	320
Db	1098	ATGATCATCATGGGATGGCCCTGAGATCCAGAGCGGTGAGGATCATCAAGGGGGCA	1157
Oy	321	ProValValGluProSerAsnLysPhePheTrpPheHISArgProAspTrpValLeuPhe	340
Db	1158	CCCGTGGTCAAGCCCAAGAAAGTCTCTGTGTTCACAGCGCGCGAGTGGGTCTCTTC	1217
Oy	341	PheIleHISLeuThrLeuPheGluHISAsnAlaPheGluMetAlaHISLysPheValTrpThVal	360
Db	1218	TTCAATACACTGACGCTGTTCAGAAAGCGTTTCAGATGGCAATTTCTGTGAGACAGTG	1277
Oy	361	AlaThrProGlyLeuLysLysCysPheHISMetHISIleGlyLeuSerIleMetLysVal	380
Db	1278	GGCAGCGCGGCTTGAAGACTCTTTCATATGAACATGGGCTAGCATCATGAAGCTC	1337
Oy	381	ValLeuGlyLeuAlaLeuGluInPheLeuCysSerTYrIleThrPheProLeuTYrAlaLeu	400
Db	1338	GTGCTGGGCTGGCTCTCCAGTCTGTGGAGTACATCATCTTCCCTCTACGGCTCA	1397
Oy	401	ValThrgLMetGlySerAsnMetLysArgSerIlePheAspGluGluThrAlaLysAla	420
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Oy	421	LeuThrasnTrpArgAsnThrAlaLysGluLysLysValArgAspThrasMetLeu	440
Db	1458	CTGACCAACTGGCGGAACCGCCCAAGGAAGAGTCCGAGACAGGACATGCTG	1517
Oy	441	MetAlaGluMetIleGlyAspAlaThrProSerArgGlyThrSerProMetProSerArg	460
Db	1518	ATGGCGAGATGATGGCGGACAGCAACCCAGCGGACGTCCTGCTAGCCGG	1577
Oy	461	AlaSerSerProValHISLeuLeuHISLysGlyMetGlyArgSerAspAspProGluSer	480
Db	1578	GGCTCATCGCGGTGCACCTGCTTCAGAAAGGCAATGGAGGTGATGATCCCAAGAC	1637
Oy	481	AlaProThrSerProArgThrMetGluGluAlaArgAspMetTYrProValValAla	500
Db	1638	GCACCGACCTCGCCAAAGACCATGGAGAGGCTAGGACATGACCGGTTGTGTGGCG	1697
Oy	501	HISProValHISArgLeuAsnProAlaSPArgArgArgSerValSerSerAlaLeu	520
Db	1698	CATCTGTACACAGACTTAATCTGTCTACAGGCGAGGTGCGTCTTTCATCAGCCCTC	1757
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Db	1758	GATGCGAGATCCCGACGACAGATTTTCTTTCAGCCAGGCA	1799
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DEFINITION	Sequence 2 from Patent WO9804586.		Linear
ACCESSION	A92828		
VERSION	A92828.1	GI:6741365	
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	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	Poideae; Triticeae; Hordeum.		
REFERENCE			
AUTHORS	1 (bases 1 to 1602)		
TITLE	Panstruga, R. and Bueschges, R.		
JOURNAL	POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN		
	PLANTS		
	Patent: WO 9804586-A 2 05-FEB-1998;		
	INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)		
FEATURES			
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Best Local Similarity:	89.20%	Mismatches:	33
Query Match:	87.43%	Indels:	4
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US-09-857-896A-32 (1-534) x A92828 (1-1602)			
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Qy 467 LeuLeuHisLysGlyMetGlyArgSerAspAspProGlnSerAlaProThrSerProArg 486
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RESULT 8
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DEFINITION Sequence 7 from Patent W09804586.
ACCESSION A92833
VERSION A92833.1 GI:6741370
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triliceae; Hordium.
REFERENCE
1 (bases 1 to 1917)
AUTHORS Panstruga, R. and Bueschges, R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
PLANTS
JOURNAL Patent: WO 9804586-A 7 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUCA RALPH (GB)
FEATURES
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Best Local Similarity: 89.20% Mismatches: 33
Query Match: 87.43% Indels: 4
DB: 6 Gaps: 3
US-09-857-896A-32 (1-534) x A92833 (1-1917)
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 VERSION 283834.1 GI:1877220
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 SOURCE Hordeum vulgare subsp. vulgare.
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 1917)
 Bueschges, R., Hollricher, K., Panstruga, R., Simons, G., Wolter, M.,
 Fritjers, A., van Daelen, R., van de Lee, T., Diergaarde, P.,
 Groenendijk, J., Toepesch, S., Vos, P., Salamini, F. and
 Schulze-Lefert, P.
 The barley Mlo gene: a novel control element of plant pathogen
 resistance
 JOURNAL Cell 88 (5), 695-705 (1997)
 MEDLINE 97207016
 PUBMED 9054509
 2 (bases 1 to 1917)
 Panstruga, R.
 Direct Submission
 Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury
 Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK
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ACCESSION AF361933
VERSION AF361933.1 GI:15290590
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QY 142 HisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrPlys 161
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QY 342 IleHisLeuThrLeuPheGlnAsnAlaPheGluMetAlaHisPheValTrpThrValAla 361
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DB 1147 CCGACCTCGCCCAAGACCATGAGAGAGGCTTGGAGCACTGTACCCGGTGTGGTGGCAT 1206
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DEFINITION

ACCESSION AF384030
VERSION AF384030.1 GI:15290604
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group).
Oryza sativa (indica cultivar-group).
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
Devoto, A., Hartmann, H. A., Piffanello, P., Elliott, C., Simmons, C.,
Taramino, G., Goh, C.-S., Cohen, F. E., Schultze-Lefert, P. and
Panstruga, R.
TITLE
Molecular phylogeny and domain-specific co-evolution of the
plant-specific seven transmembrane MLO family
JOURNAL
2 (bases 1 to 1740)
REFERENCE
AUTHORS
Elliott, C. and Schultze-Lefert, P.
TITLE
Direct Submission
JOURNAL
Submitted (22-MAY-2001) The Sainsbury Laboratory, Colney Lane,
Norwich NR4 7UH, UK
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Alignment Scores:
Pred. No.: 7.08e-176 Length: 1740
Score: 2033.50 Matches: 397
Percent Similarity: 79.78% Conservative: 45
Best Local Similarity: 71.66% Mismatches: 71
Query Match: 73.04% Indels: 41
DB: 8 Gaps: 5
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DB 77 AGGGCGTGGCGGAGACGCCGACGCGGTGGCGCGGTGGCGCGGTGGCGCGGTGGCGCGTTC 136
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DB 137 GTCCTCGTGGCATGAGACAGCGCTCCACAAAGCTCGGCATTTGGTTCCATAAGCGGGAG 196
QY 51 LysAsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValGlyPhe 70
DB 197 AAGAAAGCCATGGCGGAAGCGCTCGAAGATCAAGAGAGATTGATGCTGCGGCGCTTC 256
QY 71 IleSerLeuLeuAlaValAlaThrGlnAspProIleSerGlyIleCysIleSerGlyLys 90
DB 257 ATATCGCTGCTCTACACTGTGGCACAAGCCCATCTCCAGATATGATCATCCCGGAGCTA 316
QY 91 AlaIleSerIleMetLysProCysSerLeuProProGlySerValLys-----SerLys 108
DB 317 GCTGCCAATCATGCTGCTGCTGAAGGCAAGGCAAGATATCTCAAGGCGCTGAAGGGA 376

QY 109 TyrLysAspTyr----- 112
DB 377 AAAAAGACCATCCCGGAGGCTTCTGTACACCGGAGAAAGAGACCATCCCGG 436
QY 113 -----TyrCysAlaLysLysGlyLysValSerLeuMet 123
DB 437 TCACAGCGCGCGCGCGCGCGGAGATTACTGCGCAATGCGCAAGGCGGCGTGAATG 496
QY 124 SerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaValPheHisVal 143
DB 497 TCATCGCGCGCGCGCACACGCTGCACATATTCATTTTCGCTCGCGGCTGCCAGCTC 556
QY 144 ThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrThrLysLysTrp 163
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DB 677 ACCGATCGACATGCTTCGTGAAGACGATCTGGAGACTGTACAGCACACCTGGCTCAGA 736
QY 204 TrpValValAlaPhePheArgGlnPhePheArgSerValThrLysValAspTyrLeuThr 223
DB 737 TGGATTTGGCGGCTTCACAGCTTCCTGGCTCTGTCCACAAAGGTGACATCACTGAC 796
QY 224 LeuArgAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLys 243
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QY 244 TyrIleLysArgSerMetGlnAspAspPheLysValValGlyIleSerLeuProLeu 263
DB 857 TACATCAAGAGCTATTAGAGAGCATTTCAAAAGTTCCTGTGGCATCGCTCCCATTTG 916
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QY 284 IleSerPheIleProLeuValIleLeuLeuGlyValGlyThrLysLeuMetIleIle 303
DB 977 ATCTCTTTTGTCCACTCGTCATCTTCATCTTCATGTTGGGCAAAAGTGAATGGTTATTC 1036
QY 304 MetGluMetAlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAlaProValVal 323
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QY 324 GluProSerAsnLysPhePheThrPheHisArgProAspTrpValLeuPhePheHis 343
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QY 344 LeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValIleTrpThrValAlaThrPro 363
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DB 1277 ATATTTCATTCAGTCTTATGACAGCTACAGCACTTCCTCTTACGACATCGTCCACAG 1336
QY 404 MetGlySerAsnMetLysArgSerIlePheAspGlnIleThrAlaLysAlaLeuThrAsn 423
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FEATURES

source 1.1635 Location/Qualifiers

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/clone="MLO HOMOLOGUE"

BASE COUNT 315 a 496 c 520 g 304 t

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Best Local Similarity: 70.57% Mismatches: 83

Query Match: 70.40% Indels: 38

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QY 51 LysAsnAlaLeuAlaGluAlaLeuGluLysLysLysLysLysLysLysLysLysLys 70

DB 142 AAGAAGGCGCTGGGGGAGCGGTGGAGAAATGAGAGCGAGCTCATGCTGGGCTTC 201

QY 71 IleSerLeuLeuLeuAlaValHisLysLysLysLysLysLysLysLysLysLys 90

DB 202 ATATCCCTGCTCTCATGCTGACGAGGATCCGCTCCAGATCTGCATCTCCAAAGGAG 261

QY 91 AlaAlaSerIleMetArgProCysSerLeuProGluLysValLysSerLysLys 110

DB 262 GCCGCGAGAGATGCTCCGTCGACAGGCTTACAGCGCGCGCGGTGGCAAGGACAG 321

QY 111 AspTrpTrp 113

DB 322 GACAAATCACCGAGGCTTCTGCTCCAAAGCGAGAGCCAGCCAGCCGCGTCTG 381

QY 114 -----CysAlaLysLysGlyLysValSerLeuMetSerThr 125

DB 382 GCTGCCCGCGCGAGATGAGCTGCGCCAAACAGGGAGAGTGGCGCTGATGTCAGCG 441

QY 126 GlySerLeuHisGluLeuHisLysLysLysLysLysLysLysLysLysLys 145

DB 442 GGAAGCATGACCACTGACATATCTCATCTGCTGCGCGCTCTCCAGCTCTGTAC 501

QY 146 SerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrpLysLysTrpGluThr 165

DB 502 AGCGTGTACCATGACCTTAAGCGGTCTCAAAATGAGCAATGGAGAGTGGAGTGG 561

QY 166 GluThrAlaSerLeuGluThrGlnPheAlaAsnAspProAlaArgPheArgPheHis 185

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QY 186 GlnThrSerPheValLysArgHisLysLysLysLysLysLysLysLysLysLys 205

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QY 206 ValAlaPhePheArgGlnPhePheArgSerValThrLysValAspTrpLeuThrLeuArg 225

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QY 446 GlyAspAlaThrProSerArgGlyThrSerPrometProSerArgAlaSerProVal 465

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QY 526 SerAlaAspPheSerPheSer 532

DB 1603 GGTGCAGATTTGGCTTCAGC 1623

RESULT 14

AF388195 1894 bp mRNA linear PLN 17-APR-2002

LOCUS AF388195

DEFINITION Oryza sativa MLO (MLO) mRNA, complete cds.

ACCESSION AF388195

VERSION AF388195.1 GI:14718603

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (indica cultivar-group).

Oryza sativa (indica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehretoidae; Oryzaceae; Oryza.

1 (bases 1 to 1894)

Kim,M.C., Panstruga,R., Elliott,C., Muller,J., Devoto,A.,

Yoon,H.W., Park,H.C., Cho,M.J. and Schulze-Lefert,P.

Calmodulin interacts with MLO protein to regulate defence against

mlidew in barley
Nature 416 (6879), 447-451 (2002)
MEDLINE
21918680
PUBMED
11919636
2 (bases 1 to 1894)
REFERENCE
Kim, M.C., Lee, S.H., Kim, J.K., Chun, H.J., Kim, J.C., Heo, W.D.,
Chung, W.S., Choi, M.S., Park, C.Y., Yoon, H.W. and Cho, M.J.
AUTHORS
TITLE
Isolation and characterization of M10 homolog in rice
JOURNAL
Unpublished
3 (bases 1 to 1894)
REFERENCE
Kim, M.C., Lee, S.H., Kim, J.K., Chun, H.J., Kim, J.C., Heo, W.D.,
Chung, W.S., Choi, M.S., Park, C.Y., Yoon, H.W. and Cho, M.J.
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (01-JUN-2001) Biochemistry, Gyeongsang National
University, Gazeo-dong 900, Chinju 660-701, Korea
FEATURES
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DB 223 GTCCTCGTCGCATGAGACAGCGGCTCCACAACGCTGCGCATTTGTTCAATAGCGGGAG 282
QY 51 LysAsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValGlyPhe 70
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DB 343 ATATCGCTGCTCTCATCTGGACAAACGCCCATCTCCAAAGATATGATCCCGCATCA 402
QY 91 AlaAlaSerIleMetArgProCysSerLeuProGlySerValLys-----SerLys 108
DB 403 GCTGCCAACAATCATCTGCTCGTCAAGGCAAGGCAAGATATCTCAAGGCGCTAAGGCA 462
QY 109 TyrLysAspTyr-----TyrLys-----TyrLys-----TyrLys----- 112

DB 463 AAAAAGACCATGCGCGAGGCTTCTGTGATACCGGAGAAAGAGACCATGCGCGG 522
QY 113 -----TyrCysAlaLysValGlyLysValSerLeuMet 123
DB 523 TCACGTGCGCGCGCGCGCGCGGAGGATTAAGTCTGCGGCAATCGCGCAAGGTGGCCTATG 582
QY 124 SerThrGlySerLeuHisGlnLeuHisIlePheIlePheValAlaValPheHisVal 143
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DB 643 ACCTACTGCGCTTCACTACCATGSGGTTTAGCGCGCTCAAAATGAAAGATGAAAGATGG 702
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DB 763 ACCGATACAGCTGCTTCTGTGAGGCGCATGCGGATCTGCATCTCAAGACCCCTGGGCTC 822
QY 203 ArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLysValAspTyrLeu 222
DB 823 AGATGATCGTATGATCTTTCAGCGAGTCTTGTGGTCCGTCACCAAGGTGACTACTTC 882
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QY 243 LysTyrIleLysArgSerMetGluAspAspPheLysValValAlaGlyIleSerLeuPro 262
DB 943 AAATACATCAAGAGGCTTGTGAGACACACTTCAAAGTTCTGTCGATCAGCCTCCCT 1002
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QY 283 TrpIleSerPheIleProLeuValIleLeuLeuGlyValGlyThrLysLeuGluMetIle 302
DB 1063 TGGATCTCTTTTCTCTCTCATCATCTGTTGTTAGTGGACCAAGCTGACAGTGGTG 1122
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QY 403 GlnMetGlySerAsnMetLysArgSerIlePheAspGluIleGlnThrAlaLysAlaLeuThr 422
DB 1423 CAGATGGATCGAACAATGAAGAACAATCTTCAAGAGACAAACGATGAAGCGCTGATG 1482
QY 423 AsnTrpArgAsnThrAlaLysGluLysLysValAlaArgAspThrAspMetLeuMetAla 442
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QY 443 GlnMetIleGlyAsp---AlaThrProSerArgGlyThrSerProMetProSerArgAla 461
DB 1543 CAGATGACGCTGACTTTCGAGCGCGGCG-----TCGAGCGGCTC 1584

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: November 18, 2002, 15:39:43 ; Search time 252 Seconds

(without alignments)
4772.092 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
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Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2784	100.0	1711	21	Wheat Mlo homolog
2	2777	99.7	1692	20	Wheat Mlo fungal r
3	2777	99.7	1693	22	Nucleotide sequenc
4	2740	98.4	1868	20	Wheat Mlo fungal r
5	2740	98.4	1868	20	Nucleotide sequenc
6	2680	96.3	1886	22	Wheat Mlo fungal r
7	2680	96.3	1886	22	Nucleotide sequenc
8	2434	87.4	1602	19	Hordeum vulgare cv
9	2428	87.2	1917	19	Hordeum vulgare ML
10	1946	69.9	1635	19	Hordeum vulgare ML
11	1821	65.4	2425	19	Hordeum vulgare ML
12	1737.5	62.4	1611	19	Hordeum vulgare ML
13	1536.5	55.2	4105	19	Oryza sativa MLO g
14	1276.5	45.9	1935	20	Hordeum vulgare ML
15	1276.5	45.9	1935	20	Arabidopsis thalia
16	1276.5	45.9	2148	21	Nucleotide sequenc
17	1208.5	43.4	2096	19	Arabidopsis thalia
18	1201	43.1	1815	21	Hordeum vulgare ML
19	1201	43.1	1815	20	Maize MLO6 protein
20	1195	42.9	2030	21	Zea mays SCLBr pro
21	1160.5	41.7	2197	20	Maize MLO2 protein
22	1160.5	41.7	2197	22	Arabidopsis thalia
23	1149.5	41.3	1782	20	Nucleotide sequenc
24	1149.5	41.3	1782	22	Arabidopsis thalia
25	1120	40.2	678	21	Nucleotide sequenc
26	1110.5	39.9	7175	19	Oryza sativa MLO g
27	1069	38.4	1938	21	Wheat Mlo homolog
28	962	34.6	1745	21	Soybean Mlo homolo
29	958	34.4	563	21	Soybean Mlo homolo
30	931.5	33.5	1880	19	Arabidopsis thalia
31	927.5	33.3	1811	20	Arabidopsis thalia
32	927.5	33.3	1811	22	Nucleotide sequenc
33	927.5	33.3	1811	22	Nucleotide sequenc
34	925	33.2	1666	21	Oryza sativa MLO g
35	911	32.7	1496	21	Wheat Mlo homolog
36	902.5	32.4	1798	21	Wheat MLO8 protein
37	902	32.4	1725	20	Zea mays SCLBr pro
38	798	28.7	1869	21	Maize MLO3 CDNA.
39	798	28.7	1869	22	Maize monogenic d1
40	770.5	27.7	1660	21	Maize MLO7 protein
41	752	27.0	845	21	Maize MLO1 protein
42	745.5	26.8	1040	20	Zea mays SCLBr pro
43	741	26.6	1841	21	Maize MLO4 protein
44	736	26.4	1831	20	Zea mays SCLBr pro
45	723.5	26.0	960	21	Soybean Mlo homolo

ALIGNMENTS

RESULT 1
AAAS2715
ID AAAS2715 standard; cDNA; 1711 bp.
XX
AC AAAS2715;
XX
XX 27-OCT-2000 (first entry)
XX
DE Wheat Mlo homolog putative coding sequence #4.
XX
XX Wheat; Mlo homolog; disease resistance; ss.
XX
OS Triticum aestivum.
XX
FH Key
FT CDS
FT
FT Location/Qualifiers
FT /*tag= a
FT /product= "Mlo homologue"

XX MO200036110-r2.
PN
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99MO-US30181.
XX
PR 18-DEC-1998; 98US-0112737.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX
XX WPI: 2000-431590/37.
DR P-PSDB; AAB01805.
XX
PT New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT creating transgenic plants with altered levels of disease resistance -
XX
XX Claim 2; Page 64; 79pp; English.
XX
CC The present sequence is a putative coding sequence for a Mlo homologue
CC from wheat. It was identified by searching a root and leaf cDNA library
CC for sequences encoding proteins similar to Mlo from *Hordeum vulgare*
CC (barley) and *Arabidopsis thaliana*. Mlo confers resistance to *Erysiphe*
CC graminis f. sp. hordei upon the plant, and its inactivation leads to the
CC plating of disease resistance even if the pathogen is not present. The
CC gene and protein can be used to create transgenic plants which have
CC increased disease resistance, as well as allowing researchers to find
CC other resistance-conferring genes and proteins.
SQ
SQ Sequence 1711 BP; 377 A; 505 C; 473 G; 356 T; 0 other;

Alignment Scores:
Pred. No.: 2,26e-274 Length: 1711
Score: 2784.00 Matches: 534
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
DB: Gaps: 0

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DB 1 ATGGCGGAGGACTACGATACCCCGCGCGAGCGCTGCCGAGACGCCGCTGGCGG 60
QY 21 ValAlaLeuValPheAlaValMetIleIleValSerValLeuGluHisAlaLeuHis 40
DB 61 GTGGCGCTGCTGCGCGATGATCATCGTGTCCGCTCTCGTGGAGCAAGCGGCTCCAC 120
QY 41 LysLeuGluHisTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
DB 121 AAGCTGGCCATTGGTTCCACAGCGGACAGAACGCCGCTGGCGAGCGCTGGAGAG 180
QY 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuAlaValThrGlnAsp 80
DB 181 ATCAAAAGCGAGCTGATCTGTGGGTTTCATCTGCTGCTGCGCGTACGACGAGAC 240
QY 81 ProIleSerGlyIleCysIleSerGluLysAlaAlaSerIleMetArgProCysSerLeu 100
DB 241 CCAATCTCCGGGATATGATCTCCGAGAGGCCGCCAGATCATGGCCCTCGACGCTG 300
QY 101 ProProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysLysGlyLysVal 120
DB 301 CCCCCTGGTTCCGTCAGAGCAAGTACAAAGACTACTACTGCGCCAAAGGCGCAAGGTG 360
QY 121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal 140
DB 361 TCCGTAATGTCACGGGAGGCTTCACACCACTCCACATATTATTTGTTGTCGCCGTC 420
QY 141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrp 160

DB 421 TTCATGTACACCTACAGCGGTATCATGAGCTCTAAAGCGGTCTCAAAATGAGGACATGG 480
QY 161 LysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAspProAlaArg 180
DB 481 AAGAAATGGGAGACAGACAGCCGCTCTGGAAATACAGATGCAAAATGATCTCGCCGG 540
QY 181 PheArgPheThrHisGlnThrSerPheValLysArgHisLeuGlyLeuSerSerThrPro 200
DB 541 TTCGCGTTACGACGACAGCGCGTGTGTAAGCGGACCTGGCGCTCCACAGACCCCC 600
QY 201 GlyLLeaArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLysValAsp 220
DB 601 GGCACTAGATGGGTGGGTGGCTTCTTCAGGCAAGTTCTTCAGTGGCTGTACCAAGGTGAC 660
QY 221 TyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAsp 240
DB 661 TACCTACCCCTGAGGCGACGCTTCATCAACCGCATTTCTCCATACAGCAAGTTGTGAC 720
QY 241 PheHisLysTyrIleLysArgSerMetGluAspAspPheLysValValValGlyIleSer 260
DB 721 TTCACAGATACCTCAAGAGGTGCTATGGAGGACGACTTCAAAGTGTGCTTGCAATACG 780
QY 261 LeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThr 280
DB 781 CTCCCGCTGGTGGTGGCGATCCTCACCTCTTCGTGATATGACGGGATCGCAGC 840
QY 281 LeuThrTrpIleSerPheIleProLeuValIleLeuLeuCysValGlyThrLysLeuGlu 300
DB 841 CTCACCTGGATTCTTTCATCCCTCTCTCATCTCTTGTTGTTGGAAACCAAGCTGGAG 900
QY 301 MetIleIleMetGluMetAlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAla 320
DB 901 ATGATCATCATGAGAGATGGCCCTGAGAGATCCAGAGACCGGGCGGCTCATCAAGGGGCG 960
QY 321 ProValValGluProSerAsnLysPheThrPheHisArgProAspTrpValLeuPhe 340
DB 961 CCGGTGTTAGGCGCAGCAACAAGTTCTTGTTGTTCCACCGCCGACGGGTGCTCTGTC 1020
QY 341 PheIleHisLeuThrIleuPheGlnAsnAlaPheGlnMetLanHisPheValTrpThrVal 360
DB 1021 TTCAATACACCTGACGCTGTGTCAGAAATCGTTGATGAGACATTTGCTGTGGACAGTG 1080
QY 361 AlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
DB 1081 GCCACGCCCGGCTTGAAGAAATGCTTCATATGCACATCGGTGTGAGCATGAGAGTTC 1140
QY 381 ValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrIleThrPheProLeuThrAlaLeu 400
DB 1141 GTGCTGGGGCTGGCTCTTCAATTCTCTGACGTAATACCTTCCCTCTACGCGCTC 1200
QY 401 ValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThrAlaLysAla 420
DB 1201 GTCAACACGATGGGATCGAAACATGAAGAGGTCATCTTCAGACAGACAGCGCCAAAGCG 1260
QY 421 LeuThrAsnTrpArgAsnThrAlaLysGluLysLysValAlaArgSerPheAspMetLeu 440
DB 1261 CTGACCAACTGGGGGAACACGGCCAAAGGAGAAAGAGGTGCGAGAACAGGACATGCTG 1320
QY 441 MetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSerProMetProSerArg 460
DB 1321 ATGGCGCAGATGATGGCGGACCGGACCGCCAGGAGGACAGTCCGATGTGATAGCGCG 1380
QY 461 AlaSerSerProValHisLeuMetHisLysGlyMetGlyLysArgSerAspAspProGlnSer 480
DB 1381 GCTTCGTACCGGGGCACTGCTTACAAAGGAGCATGGGAGGATCCAGCATCCCAAGAC 1440
QY 481 AlaProThrSerProArgThrMetGluGlnAlaArgAspMetLysProValValValAla 500
DB 1441 GCGCGGACCTCGCCAAAGGACCAATGAGAGAGCTGAGGACATATGACCCGGTTGTGGTGG 1500
QY 501 HisProValHisArgLeuAsnProAlaAspArgArgSerValSerSerSerAlaLeu 520
DB 1501 CATCCCGTGACAGACTAAATCTGTGACAGGGGAGGTGGGTCTTCTGTGGGCACTTC 1560

QY 521 AspalaspilproserAlaaphaserPheserGingly 534
|||||
DB 1561 GATGCCGACATCCCGACGATTTTCTTCAGCCAGGGA 1602
RESULT 2
AAZ30410
ID AAZ30410 standard; DNA; 1692 BP.
XX
AC AAZ30410;
XX
XX 21-DEC-1999 (first entry)
DB wheat Mlo fungal resistance gene Trm102.
XX
XX Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KM papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW Mlo; Erysiphe graminis; powdery mildew; ss.
XX
XX Triticum sp.
XX
XX Key Location/Qualifiers
FT 1..1605
FT CDS /*tag= a
FT /product= "fungal resistance protein Mlo2"
FT /transl_except= (pos:502..504, aa:Xaa)
FT /note= "Xaa = unknown"
XX
XX WO947552-A2.
XX
XX 23-SEP-1999.
XX PD
XX 17-MAR-1999; 99WO-EP01779.
XX PF
XX 17-MAR-1998; 98US-0042763.
XX PR
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.
XX
XX Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX WPI; 1999-571820/48.
XX DR P-PSDB; AAY26967.
XX
XX New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 2; Page 63-65; 102pp; English.
XX
XX This sequence represents the coding region for the wheat fungal
CC resistance gene Trm102. The Mlo protein confers resistance to fungal
CC pathogens by stimulating the formation of large cell wall appositions,
CC designated papillae, at the contact site with the fungal pathogen.
CC These papillae mainly contain callose, but also contain carbohydrate,
CC phenols and proteins and are used to prevent penetration of the fungal
CC hyphae into the plant. The new Mlo sequences are used to generate
CC transgenic plants resistant to fungal pathogens, especially Erysiphe
CC graminis (powdery mildew).
XX
SQ Sequence 1692 BP; 360 A; 505 C; 471 G; 355 T; 1 other;
Alignment Scores:
Pred. No.: 1,15e-273 Length: 1692
Score: 2777.00 Matches: 532
Percent Similarity: 99.81% Conservative: 1
Best Local Similarity: 99.63% Mismatches: 1
Query Match: 99.75% Indels: 0
DB: Gaps: 0
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|||||

DB 1 ATGGCGGAGACTACGAGTACCCCCGGCGCGGACGCTGCGGAGACCGCGTCTGGCGG 60
QY 21 ValAlaLeuValPheAlaValMetIleIleValSerValLeuLeuGlnHisAlaLeuHis 40
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DB 61 GTGGCGCTGCTCTTCCGCGCATGATCATCTGCTCCGCTCTCGAGACGCGGCTCCAC 120
QY 41 LysLeuGlyHisTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
|||||
DB 121 AAGCTCGGCCATTGTTGTTCCACAGCGGCACAAAGAGCGCTGGCGAGCGCTGGAGAAG 180
QY 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuAlaValThrGlnAsp 80
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DB 181 ATCAAGCGGAGCTGATGCTGGTGGGCTTCATCTGCTGCTGCTGCGCGAGCAGAGC 240
QY 81 ProIleSerGlyIleCysIleSerGlyLysAlaIleSerIleMetArgProCysSerLeu 100
DB 241 CCATCTCCGGGATATCATCTCCGAGAAAGCGCGCACATCATGCGCGCTGACGCTG 300
QY 101 ProProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysGlyLysVal 120
|||||
DB 301 CCCCTGGTTCGTCAGAGCAAGTCAAAAGACTACTCGCCCAAAAGGCAAGGTG 360
QY 121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal 140
DB 361 TCGCTATGTCACAGGGGACCTTGACACAGCTCCCATGTTCACTTCTGCTGCGCGTC 420
QY 141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrp 160
|||||
DB 421 TTCATGTCACCTACACGCTCATCATCAAGCTCTAAAGCCCTCAAAATGAGACATGG 480
QY 161 LysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAspProIleArg 180
DB 481 AAGAAATGGAGACAGAGACGACCGCTCTTGGAAATACAGTTCCGAATATATCTCGCGG 540
QY 181 PheArgPheThrIleGlnThrSerPheValLysArgHisLeuGlyLeuSerThrPro 200
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QY 201 GlyIleArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLysValAsp 220
DB 601 GGCATCAGATGGGTGGTGGCTCTTCAAGGAGCTTCTTCAAGTGCATCAAGGTGAGC 660
QY 221 TyrLeuThrLeuAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAsp 240
DB 661 TACCTCACCCTGAGGAGGCTTCATCAACGCGGATTTGCGATTAACGACAAAGTTCCAC 720
QY 241 PheHisLysTyrIleLysArgSerMetGlnAspAspPheLysValValGlyLysSer 260
DB 721 TTCACAAAGTACATCAAGAGGTCCATGGAGGACGACTTCAAAAGTCGCTTGATCAGC 780
QY 261 LeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThr 280
DB 781 CTCGCGGTGGTGGTGGGAGTCCATCAACGCGCTTCTTCAATATTAACGGGATCGGCGC 840
QY 281 LeuThrTrpIleSerPheIleProLeuValIleLeuLeuCysValGlyThrLysLeuGlu 300
DB 841 CTCACCTGAGATTCTTCACTCCGTCGATCCCTTGGTGGTGGAAACCAAGTGGAG 900
QY 301 MetIleLeuMetGlnMetAlaLeuGluIleGlnAspArgLysSerValIleLysIleVal 320
DB 901 ATGATCATCATGAGAGTGGCTGGAGATCCAGAGACGGGCGAGCTCATCAAGGGGCGG 960
QY 321 ProValValGluProSerAsnLysPheThrPheHisArgProAspTrpValLeuPhe 340
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QY 341 PheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValThrProVal 360
DB 1021 TTCAATACACTGACGCTGTTCCAGAAATCGTTTACATGACACATTTGCTGGACAGTG 1080
QY 361 AlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
DB 1081 GCCACGCCCGCTTGAAGAAATGCTTCATATGACATCGCTGAGCATCATGAAGTGC 1140

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DB 1141 GTGGTGGGGCTGGCTCTTCAGTTCCTGTCAGACTATATACCTTCCCTACCGCTC 1200
QY 401 ValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGlnThrAlaLysAla 420
DB 1201 GTCCACACAGATGGGATCGAATGAAAGAGTTCATCTTCACAGACGAGCGCAAGGCG 1260
QY 421 LeuThrAsnThrPargAsnThrAlaLysGluLysLysValArgAspThrAspMetLeu 440
DB 1261 CTGACCAACTGGCGGAACACGGCCAAAGAGAAAGAGTCCGACACAGCACTGGCTG 1320
QY 441 MetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSerProMetProSerArg 460
DB 1321 ATGGCGCAGATGATGGCGGACGGCCAGCGCCAGCGACGTCGCGATGCGCTAGCCGG 1380
QY 461 AlaSerSerProValHisLeuLeuHisLysGlyMetGlyArgSerAspAspProGlnSer 480
DB 1381 GCTTGTCCACCGGTGCACCTGCTCCAAAGGACATGGACGGTCCGACGATCCCAAGAC 1440
QY 481 AlaProThrSerProArgThrMetGluGluAlaArgAspMetTyrProValValAla 500
DB 1441 GCGCGACCTCGCCAAAGACATGAGGAGGCTAGGACATGACCGGTTGGTGGCG 1500
QY 501 HisProValHisArgLeuAsnProAlaAspArgArgArgSerValSerSerAlaLeu 520
DB 1501 CATCCCGTGCACAGACTAAATCTCTGCTGACAGGCGAGTGGCTCTTCTGTCGGCCTC 1560
QY 521 AspAlaAspIleProSerAlaAspPheSerPheSerGlnGly 534
DB 1561 GATGCCGACATCCCGACGCGATTTTCTTCCTTCAAGCCAGGGA 1602
RESULT 3
AAF24584
ID AAF24584 standard; DNA; 1693 BP.
AC AAF24584;
XX
XX 20-APR-2001 (first entry)
XX
XX Nucleotide sequence of the wheat Mlo protein TmMlo2.
XX
XX Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
XX powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
XX
XX Triticum sp.
XX
XX Location/Qualifiers
FH Key 1..1605
FT /*tag= a
FT /product= "Mlo protein"
FT /transl_except= "(pos: 502..504, aa: 'Xaa'"
FT /note= "Xaa is an unspecified amino acid"
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XX
XX 28-DEC-2000.
XX
XX 16-JUN-2000; 2000MO-EP05576.
XX
XX 18-JUN-1999; 99US-0336112.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;
XX Vernooij BT, Levin JZ, Helfetz PB, Patton DA, Que Q;
XX WPI: 2001-112311/12.
XX P-PSDB; AAB31251.
XX
XX Novel polynucleotide which encodes Mlo protein from wheat, useful for
```

PF producing fungal resistant plants, in particular wheat plant -
XX
XX Claim 2: Page 92-94; 128bp; English.

XX The present sequence encodes a Mlo protein. Mlo proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC Mlo proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildew). In barley, mutations at the Mlo
CC locus are responsible for a plant resistant pathotype. The mechanism
CC of Mlo resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding Mlo proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.

XX Sequence 1693 BP; 360 A; 505 C; 472 G; 355 T; 1 other;

Alignment Scores:

Pred. No.:	1,15e-273	Length:	1693
Score:	2777.00	Matches:	532
Percent Similarity:	99.81%	Conservative:	1
Best Local Similarity:	99.63%	Mismatches:	0
Query Match:	99.75%	Indels:	0
DB:	22	Gaps:	0

us-09-857-896a-32 (1-534) x AAF24584 (1-1693)

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DB 1 ATGGCGGAGAGCTACGAGATACCCCGCGCGGACCTCCGGAAGCCCTCTGGGCG 60
QY 21 ValAlaLeuValPheAlaValMetIleIleValSerValLeuLeuGlnHisAlaLeuHis 40
DB 61 GTGGCGCTGCTCTGCGCGTATGATCATGTCTCCGCTCTCTGAGACAGCGCTTCCAC 120
QY 41 LysLeuGluYHisTyrPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
DB 121 AAGCTGGCCATTGGTCCACACAGCGGACAAAGAGCGCTGGGAGGCGCTGGAGAG 180
QY 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuLeuAlaValThrGlnAsp 80
DB 181 ATCAAGACGAGCTGATGCTGTGGGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 81 ProIleSerGlyIleCysAlleSerGlyAlaAlaAlaSerIleMetArgProCysSerLeu 100
DB 241 CCATCTCCGGATATGATGATCTCCGAGAAAGCCGACGATATGCGGCTGAGCGCTG 300
QY 101 ProProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysLysGlyLysVal 120
DB 301 CCCCTGTGCTCCGTCAGAGCAAGTACAAAGACTACTGCGCCAAAGAGGCAAGGTG 360
QY 121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal 140
DB 361 TCGGTATATGTCACAGCGGAGGCTTGACACAGTGCACATGTATCTGCTGCGCGCTC 420
QY 141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrThr 160
DB 421 TTCATGTACCTACAGCGCTCATCTATGCTCTTAAGCGCTCTAATAATAGAGCATGG 480
QY 161 LysLysTrpGluThrGluThrAlaSerLeuGluLysGlnPheAlaAsnAspProAlaArg 180
DB 481 AAGAAATGGGAGAGACAGACGCGTCTGGAATACAGATGCGCAATGATCTGCGCGG 540
QY 181 PheArgPheThrHisGlnThrSerPheValLysArgHisLysGluLysSerSerThrPro 200
DB 541 TTCGCTTCACGACGACAGCGTCTGTGAAGCTACCTGGGCGCTCTCCAGGACCCG 600
QY 201 GlyIleArgTyrValValAlaPhePheArgGlnPhePheArgSerValThrLysValAsp 220
DB 601 GGCATCAGATGGGTGGCTCTTTCAGGAGAGTCTTCAGTGGGTGATCCAAAGGTGAG 660
QY 221 TyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAsp 240
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 Qy 261 LeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAspGlyTlGlyThr 280
 Db 781 CTCGGCTGTGGTGTGGCGATCTCCACCTCTCTCTTCATATTGACGGATCGGCACG 840
 Qy 281 LeuThrTrpLeuSerPheIleProLeuValIleLeuLeuCysValGlyThrLysLeuGlu 300
 Db 841 CTCACCTGGATTCTTTCATCCCTCTGTCATCCCTCTGTGGTGGAAACCAACTGGAG 900
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 Qy 321 ProValValGluProSerAsnLysPhePheTrpPheHisArgProAspTrpValLeuPhe 340
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 Qy 341 PheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValTrpThrVal 360
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 Qy 361 AlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
 Db 1081 GCCACGCCGGCTGACAGAAATGCTTCATATGCAATGAGTCTGATGACATATGAAAGTTC 1140
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 Db 1141 GTCTGGGGCTGGCTTCACGTCTCTGACGTATATACCTTCCCTGACGGCTC 1200
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 Db 1321 ATGGCGCAGATGATCGGCGACGCGCCACGCGAGGAGACCTCCCATCTACGCCG 1380
 Qy 461 AlaSerSerProValHisLeuLeuHisLysGlyMetGlyArgSerAspAspProGlnSer 480
 Db 1381 GCTTCGTACCGGTGACCTGCTTCACAAAGGATGGACGGTCCGACGATCCCAAGAC 1440
 Qy 481 AlaProThrSerProArgThrMetGlnGluAlaArgAspMetTyrProValValAla 500
 Db 1441 GCCCGACCTCCCAAGGACCATGGAGAGGCTAGGACATGACCGGTTGTGTGGCG 1500
 Qy 501 HisProValHisArgLeuAsnProAlaAspArgArgSerValSerSerSerAlaLeu 520
 Db 1501 CATCCGCTGACAGACTAAATCTGCTGACAGCGGAGGCTGGTCTTCTGCTGGCAGTTC 1560
 Qy 521 AspAlaAspIleProSerSerAlaAspPheSerPheSerGlnGly 534
 Db 1561 GATGCCGACATCCCAAGCGCAGATTTCCTTCAGCCAGCA 1602
 RESULT 4
 AAZ30409
 ID AAZ30409 standard; DNA; 1868 BP.
 AC AAZ30409;
 XX
 XX 21-DEC-1999 (first entry)
 XX
 XX Wheat MLO fungal resistance gene TrMLol.
 DE
 XX
 XX Consensus: resistance; fungus; pathogen; wheat; cell wall; apposition;

KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
 KM MLO; Erysiphe graminis; powdery mildew; ss.
 OS Triticum sp.
 FH Key Location/Qualifiers
 FT CDS 176..1780
 FT /*tag= a
 FT /product= "fungal resistance protein MLO1"
 XX
 XX W09947552-A2.
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99MO-EP01779.
 XX
 PR 17-MAR-1998; 98US-0042763.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
 DR MPI: 1999-571820/48.
 DR P-PSDB: AAY26966.
 XX
 PT New proteins useful for generating transgenic plants resistant to
 PS fungal infection -
 XX
 PS Claim 2; Page 58-60; 102pp; English.
 CC This sequence represents the coding region for the wheat fungal
 CC resistance gene TrMLol. The MLO protein confers resistance to fungal
 CC pathogens by stimulating the formation of large cell wall appositions,
 CC designated papillae, at the contact site with the fungal pathogen.
 CC These papillae mainly contain callose, but also contain carbohydrate,
 CC phenols and proteins and are used to prevent penetration of the fungal
 CC hyphae into the plant. The new MLO sequences are used to generate
 CC transgenic plants resistant to fungal pathogens, especially Erysiphe
 CC graminis (powdery mildew).
 CC
 SO Sequence 1868 BP; 399 A; 565 C; 521 G; 383 T; 0 other;
 Alignment Scores:
 Pred. No.: 8,15e-270 Length: 1868
 Score: 2740.00 Matches: 524
 Percent Similarity: 98.69% Conservative: 3
 Best Local Similarity: 98.13% Mismatches: 7
 Query Match: 98.42% Indels: 0
 DB: 20 Gaps: 0
 US-09-857-896A-32 (1-534) x AAZ30409 (1-1868)
 Qy 1 MetAlaGlnAspTyrGlyTrpProProAlaArgThrLeuProGluThrProSerTrpAla 20
 Db 176 ATGGCGCGACGACGACGAGTACCCCGCAGGAGGACGCGCGGAGACGCGTCTGGGCG 235
 Qy 21 ValAlaLeuValPheAlaValMetIleIleValSerValLeuLeuGlnHisAlaLeuHis 40
 Db 236 GTGGCGCTCGTCTCGCGCATGATCATCGTCTGCTCTCTGAGACACCGCTCCAT 295
 Qy 41 LysLeuGlnHisTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
 Db 296 AAGCTCGGCAATGTGTTCCACAAAGCGGCACAAAGCGGTGGCGGAGCGCTGGAGAAG 355
 Qy 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuLeuAlaValThrGlnAsp 80
 Db 356 ATCAAGGCGGAGCTCATCGGTGGGCTTCATCTCGCTGCTCCGCTGACGAGAC 415
 Qy 81 ProIleSerGlyIleCysIleSerGlnLysAlaAlaSerIleMetArgProCysSerLeu 100
 Db 416 CCCATCTCCGGGATATGATCTCCGAGAAAGCCCGCAGCATATGCGGCGCTGCAAGCTG 475

QY 101 ProProGlySerValLysSerLysTyrLysAspTyrCysAlaLysGlyVal 120
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 Db 476 CCCCTGGCTCCGTAAAGACAGTAAAGACTACTACTGCGCAACAGGGCAGG 535
 QY 121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal 140
 |||||
 Db 536 TCGCTCATGTCACGAGGCGACCTTGCACAGCTGCACATATTCATCTTCGTCGCGCTC 595
 QY 141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrp 160
 |||||
 Db 596 TTCATGTCACCTTACAGCTCATCATCAGGCTCTAACCCCTCTCAAAAATGAGAACCTCG 655
 QY 161 LysLysTrpGlnThrGlnThrAlaSerLeuGlnTyrGlnPheAlaAsnAspProAlaArg 180
 |||||
 Db 656 AAGAAATGGAGACAGAGACCGCTCCCTGGAAATACAGTTCGCGCAATGTATCTCGCGCG 715
 QY 181 PheArgPheThrHisGlnThrSerPheValLysArgHisGlnLeuSerSerThrPro 200
 |||||
 Db 716 TTCGGCTTCACGACACAGACGCTGCTTCTGAAGCGGACCTGGGCGCTCTCCAGACCC 775
 QY 201 GlyIleArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLysValAsp 220
 |||||
 Db 776 GCGCTCATAGTGGTGGCTTCTTACAGGAGTTCCTTACAGTGGTGGTACCAAGGGGAC 835
 QY 221 TyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAsp 240
 |||||
 Db 836 TACCTCACCTTGAGGCGACGCTTCATCAACGGCGCATTTGCGCATTAACACAAAGTTCCGC 895
 QY 241 PheHisLysTyrIleLysArgSerMetGluAspPheLysValValValGlyIleSer 260
 |||||
 Db 896 TTCACAAAGTACATCAAGAGGTCCATGGAGGACGAGCTTCAAAAGTCGCTGGCATAACAC 955
 QY 261 LeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThr 280
 |||||
 Db 956 CTCGGCTGTGGTGGTGGGATCTCACCCCTTCTTGACATTTGACGGGATCGGCAGC 1015
 QY 281 LeuThrTrpIleSerPheIleProLeuValIleLeuLeuCysValGlyThrLysLeuGlu 300
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 Db 1016 CTCACCTGGATTTCTTTCATCTCTCTGTCATCTCTTGTGTGGAAACCAAGCGGAG 1075
 QY 301 MetIleIleMetGluMetAlaLeuGlnIleGlnAspArgAlaSerValIleLysGlyAla 320
 |||||
 Db 1076 ATGATCATCATGAGAGATGGCCCTGGAGATCCAGGACCGGGGACGTCATCAAGGGGCGG 1135
 QY 321 ProValValGluProSerAsnLysPhePheTrpPheHisArgProAspTrpValIlePhe 340
 |||||
 Db 1136 CCGGTGGTTGAGCCAGACAAAGTCTTGTGTTCCACCCCGCAGCTGGTCTCTTC 1195
 QY 341 PheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValTrpThrVal 360
 |||||
 Db 1196 TTCATACACTGACGCTATTCGCAAAACGGCTTTCAGATGGCACAATTCGTGTGACAGATG 1255
 QY 361 AlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
 |||||
 Db 1256 GCCACGCCCGGCTTGAAGAAATGCTTCCATATGCAATCGGCTGACATCAAGAAAGGTTC 1315
 QY 381 ValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrIleThrPheProLeuTyrAlaLeu 400
 |||||
 Db 1316 GTGCTGGGGCTGGCTTTCAGTTCCTCTGACCTATATCACCTTCCGCTCTACGGCGTTC 1375
 QY 401 ValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGlnGlnThrAlaLysAla 420
 |||||
 Db 1376 GTACACAGATGGATCAAAATGAAAGTCCATCTTCGACGAGCAGAGCGCCAAAGGGG 1435
 QY 421 LeuThrAsnTrpArgAsnThrAlaLysGlyLysLysValArgAspThrAspMetLeu 440
 |||||
 Db 1436 CTGACAAACTGGCGAACACGCGCAAGGAGAAAGGTCCAGACGACGACGACGACGCTG 1495
 QY 441 MetAlaGlnMetIleGlyAspAlaThrProSerArgGlyTrpSerProMetProSerArg 460
 |||||
 Db 1496 ATGGCGCAGATGATCGCGACGCGACGCCCAAGGGGCGTGGCCCATGCTTAACCGG 1555
 QY 461 AlaSerSerProValHisLeuLeuHisLysGlyMetGlyArgSerAspAspProGlnSer 480

Db 1556 GGCTCGTCCCGACGTGCACCTCTTACAAAGGCATGGAGCGGTCCGACGATCCCAAGAC 1615
 |||||
 QY 481 AlaProThrSerProArgThrMetGlnGlnAlaArgAspMetTyrProValValAlaVal 500
 |||||
 Db 1616 ACGCCAACCTCCGCAAGGCCCATGAGAGGCTTGAAGCATTTACCGGTTGTGTGCGC 1675
 QY 501 HisProValHisArgLeuAsnProAlaAspArgArgSerValSerSerSerAlaLeu 520
 |||||
 Db 1676 CATCCAGTGCAGACTAAATCTGCTGACAGAGAAAGGTGCGTCTGCTCGCGGCACTC 1735
 QY 521 AspAlaAspIleProSerAlaAspPheSerPheSerGlnGly 534
 |||||
 Db 1736 GATGTGCACATTTCCAGCGCAGATTTTCTTCCATGCCAGGGA 1777
 |||||
 RESULT 5
 AAF24583
 ID AAF24583 standard; DNA; 1868 BP.
 AC AAF24583:
 XX
 DP 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of the wheat MLO protein TmMLO1.
 KW Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
 KN powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
 XX
 OS Triticum sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 176..1780
 FT /tag= a
 FT /product= "Mlo protein"
 PN W020007879-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000MO-EP05576.
 XX
 PR 18-JUN-1999; 99US-0336112.
 XX
 PA (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERM GBS MBH.
 XX
 PI Salmeron JM, Welislo LJ, Strawn LJ, Kramer CM, Wang HX;
 PI Vernooij BJ, Levin JZ, Heitetz PB, Patton DA, Que Q;
 XX
 DR WPI: 2001-112311/12.
 XX P-PSDB: AAB31250.
 XX
 PT Novel polynucleotide which encodes Mlo protein from wheat, useful for
 PT producing fungal resistant plants, in particular wheat plant -
 XX
 ES Claim 2; Page 88-90; 128pp; English.
 XX
 CC The present sequence encodes a Mlo protein. Mlo proteins given
 CC resistance to fungal pathogens which infect living epidermal plant cells.
 CC Mlo proteins give proteins resistance to fungal pathogens, especially
 CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
 CC locus are responsible for a plant resistant pathway. The mechanism
 CC of Mlo resistance involves the formation of large cell wall appositions,
 CC called papillae, at pathogen contact sites. Papillae mainly contain
 CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
 CC encoding Mlo proteins are useful for making transgenic plants,
 CC preferably wheat, which are resistant to fungal pathogens.
 XX
 SO Sequence 1868 BP; 399 A; 565 C; 521 G; 383 T; 0 other.
 Alignment Scores: 8,15e-270 Length: 1868
 Pred. No.: 2740.00 Matches: 524
 Score:

Percent Similarity: 98.69% Conservative: 3
 Best Local Similarity: 98.13% Mismatches: 7
 Query Match: 98.42% Indels: 0
 DB: 22 Gaps: 0
 US-09-857-896a-32 (1-534) x AAF24583 (1-1868)

0y 1 MetaLagLusPrtyrGluTyrProProAlaArGThrLeuProGluThrProSerTriPa 20
 Db 176 ATGCGGAGCAGCAGAGATACCCCGACGAGCGGTGCGGAGACGGCTCCCGGGCG 235
 0y 21 ValAlaLeuValPheAlaValMetLleIleValSerValLeuGluHisAlaLeuHis 40
 Db 236 GTGCGCCCTGCTTCGCGCTCATGATCATGCTGCTCGCTCTCGAGACGCCCTCAT 295
 0y 41 LysLeuGluHisTriPheHisLysArGHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
 Db 296 AAGCTCGGCATTTGGTTCACAAAGCGCACAAAGCGCGCTGGCGAGCGCTGGAGAG 355
 0y 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuLeuValThrGlnAsp 80
 Db 356 ATCAAGCGGAGCTCATGCTGTGGCTTCATCTCGCTGCTGCGGTACCGAGAC 415
 0y 81 ProIleSerGlyTLeGysIleSerGluLysAlaAlaSerIleMetArGProCysSerLeu 100
 Db 416 CCCATCTCCGGGATATGCATCTCCGAGAAAGCGCCAGCATCATGCGGCCCTGCAAGCTG 475
 0y 101 ProProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysGlyLysVal 120
 Db 476 CCCCGTGGCTCCGTCAGAGCAAGCAATACAAAGACTACTAGCGCCAAAGCGCAAGGCTG 535
 0y 121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal 140
 Db 536 TCGCTCATGCTCCACGGGAGAGCTTGACCACTGCACATATCATCTGCTGCTGCGCTC 595
 0y 141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArGLeuLysMetArGThrTri 160
 Db 596 TTCCATGTCACTACAGCGTCATCATATGCTTAAGCGCTCAAAATAGAAACCTGG 655
 0y 161 LysLysTriGluThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAspProAlaArg 180
 Db 656 AAGAAATGGAGACAGAAACCGCTCCCTGGAATACACTGTGCAAAAGATCCGCGCGG 715
 0y 181 PheArGpHeThrHisGlnThrSerPheValLysArGHisLeuGlyLeuSerSerThrPro 200
 Db 716 TTCCGCTTCACGACACAGACGTCGTGTGAAGCGGCACTGGGCTCTCCAGACCCCC 775
 0y 201 GlyIleArGTriValValAlaPhePheArGlnPhePheArGSerValThrLysValAsp 220
 Db 776 GCGCTCAGATGGGTGGCTGCTCTTCAGGCACTTCTTCAAGTCCGTCACCAAGCTGGAC 835
 0y 221 TyrLeuThrLeuArGAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAsp 240
 Db 836 TACCTACCTTAGGAGGAGGCTTCATCAACGGCACTTTTCCCAAAACAGCAAGTTGGAC 895
 0y 241 PheHisLysTyrLleLysArGSerMetGluAspAspPheLysValValValGlyTleSer 260
 Db 896 TTCACAAAGTACATCAAGAGGTCCATGAGAGCACTTCAAGGTGCTGGTGGATCAGC 955
 0y 261 LeuProLeuTyrCysValAlaIleLeuThrLeuPheLeuAspIleAspGlyTleGlyThr 280
 Db 956 CTCGCCCTGTGTGGTGGATCTTCACCCCTCTCTTGAACATGAGCGGATGGGACG 1015
 0y 281 LeuThrTriPheSerPheIleProLeuValIleLeuLysValGlyThrLysLeuGlu 300
 Db 1016 CTCACCTGGATTTCTTTATATCCCTCTGTCATCTCTTGTGTGGAAACCAAGCTGGAG 1075
 0y 301 MetIleIleMetGluMetAlaLeuGluIleGlnAspArGAlaSerValIleLysGlyAla 320
 Db 1076 ATGATCATCATGAGATGGCCCTGAGATCCAGAACCGGCGAGGTCATCAAGGGGGCG 1135
 0y 321 ProValValGluProSerAsnLysPhePheTriPheHisArGProAspTriPvalLeuPhe 340
 |||||||

Db 1136 CCGGTGTTGAGCCAGCACAAAGTTCTTCTGTGTTCCACCCCGCCAGCTGGCTCTTC 1195
 0y 341 PheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValTyrTriVal 360
 Db 1196 TTCTATACACTGAGCTATTCAGAAAGCGTTTCCAGATGGACATTTCTGTGGACAGTG 1255
 0y 361 AlaThrProGlyLeuLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
 Db 1256 GCCACGCCCGCTTGAAGAAATCTTCCATATGCAATGCGAGGTGGACATCATGAAGGTC 1315
 0y 381 ValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrIleThrPheProLeuTyrAlaLeu 400
 Db 1316 GTGCTGGGGCTGGCTCTTCAGTTCTCTGACACTATATCACCTTCCCGCTACGGGCTC 1375
 0y 401 ValThrGlnMetGlySerAsnMetLysArGSerIlePheAspGluGlnThrAlaLysAla 420
 Db 1376 GTACACAGATGGATCAAAACATGAAGAGCTCATCTTCGACGACAGAGGCCAAAGGCG 1435
 0y 421 LeuThrAsnTriPheAsnThrAlaLysGluLysLysValArGAspThrAspMetLeu 440
 Db 1436 CTGACAAACTGCGGAAACAGCGCCAAAGGAGAAAGAGTCCGAGACAGCATATGCTG 1495
 0y 441 MetAlaGlnMetIleGlyAspAlaThrProSerArGglyThrSerProMetProSerArG 460
 Db 1496 ATGGGCGAGATGATGGCGACAGCGGCCACCGAGGGGCTGCGCCATGCTTACCGCG 1555
 0y 461 AlaSerProValHisLeuLeuHisLysGlyMetGlyArGSerAspAspProGlnSer 480
 Db 1556 GCGCTGTCGCCAGTGACACTGCTTCAAGGGCATGAGGACGCTCGACATCCCGACAGAC 1615
 0y 481 AlaProThrSerProArGThrMetGluGluAlaArGAspMetTyrProValValAla 500
 Db 1616 ACGCCAACTCGCCAAAGGCGCATGAGAGGCTTAGAGCAATGCCGGTGTGGTGGCG 1675
 0y 501 HisProValHisArGLeuAsnProAlaAspArGArGArGSerValSerSerAlaLeu 520
 Db 1676 CATCCAGTGACAGACTAAATCTGCTGACAGAGAAAGTGTGCTGTCTGTGGCACTC 1735
 0y 521 AspAlaAspIleProSerAlaAspPheSerPheSerGlnGly 534
 Db 1736 GATGTGACATTTCCACGCGCAGATTTTCTTCAACGAGGA 1777
 RESULT 6
 AA230411
 ID AA230411 standard; DNA: 1886 BP.
 XX
 AC AA230411;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Wheat Mlo fungal resistance gene TRM103.
 XX
 KW Consensus; resistance: fungus; pathogen: wheat; cell wall; apposition;
 KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
 KW Mlo; Erysiphe graminis; powdery mildew; ss.
 XX
 OS Trifolium sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 198..1802
 FT /*tag "a
 FT /product= "fungal fusion protein M103"
 PN W09947552-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99MO-EP01779.
 XX
 PR 17-MAR-1998; 98US-0042763.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weisio LJ, Strawn LJ, Kramer CM;
XX WPI: 1999-571820/48.
DR P-PSDB; MAY26968.
XX

PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX

PS Claim 2: Page 68-70; 102pp; English.

XX This sequence represents the coding region for the wheat fungal
CC resistance gene TrM103. The M10 protein confers resistance to fungal
CC pathogens by stimulating the formation of large cell wall appositions,
CC designated papillae, at the contact site with the fungal pathogen.
CC These papillae mainly contain callose, but also contain carboxylate,
CC phenols and proteins and are used to prevent penetration of the fungal
CC hyphae into the plant. The new M10 sequences are used to generate
CC transgenic plants resistant to fungal pathogens, especially Erysiphe
CC graminis (powdery mildew).
XX

SQ Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

Alignment Scores:

Pred. No.:	1,13e-263	Length:	1886
Score:	2680.00	Matches:	513
Percent Similarity:	98.13%	Conservative:	11
Best Local Similarity:	96.07%	Mismatches:	10
Query Match:	96.26%	Indels:	0
DB:	20	Gaps:	0

US-09-857-896A-32 (1-534) x AA230411 (1-1886)

Oy 1 MetAlaGluAspTyrGluTyrProAlaArgThrLeuProGluThrProSerTrpAla 20
|||:::|||||
Db 198 ATGGCAAGAGACGAGCGGGTACCCCGGGGAGCGTGGGAGAGCGCTCTGGGG 257
Oy 21 ValAlaLeuValPheAlaValMetIleValSerValLeuLeuGluHisAlaLeuHis 40
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Db 258 GTGGCGTGTCTGCGCGTATGATCATGCTGCTGCTGCGAGCAAGCGCTCCAC 317
Oy 41 LysLeuGluHisTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
|||||
Db 318 AAGCTCGGCATGTGTTCCAAAGCGGCAAGAAAGCGGCGTGGGAGGCGTGGAGAG 377
Oy 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuAlaValThrGlnAsp 80
|||||
Db 378 ATGAAGCGGAGCTGATGCTGTGGATTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 437
Oy 81 ProIleSerGlyIleCysIleSerGlyLysAlaIleSerIleMetArgProCysSerLeu 100
|||||
Db 438 CCAATCTCGGGATATGATCTCCCAAGAGCGGCGACATCATGCGCCCTGCAAGGTC 497
Oy 101 ProProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysGlyVal 120
|||||
Db 498 GAACCGGTTCCGTAAGAGAGTACAAGAGCTACTCTGCGCCAAAGAGGCAAGGTG 557
Oy 121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal 140
|||||
Db 558 GCGCTCATGCTCAGCGGAGCGTGCACAGCTCCACATATTCATCTTCGTCAGCGCTG 617
Oy 141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrp 160
|||||
Db 618 TTCCATGTCACCTACAGCGTATCATATGAGCTTAAGCGCGTCAAGATGAGACATGG 677
Oy 161 LysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAspProAlaArg 180
|||||
Db 678 AAGAAATGGAGACAGAAACCGCTCTTGGAAATACAGATTGCGAAATGATCTGGCGG 737
Oy 181 PheArgPheThrHisGlnThrSerPheValLysArgHisLeuGluLysSerTrpPro 200
|||||
Db 738 TTCGGCTTACGACCAAGACGTGCTGTGTAAGCGGACACTGGGCTGTGTCAGACCCCC 797

Oy 201 GlyIleArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLysValAsp 220
|||:::|||||
Db 798 GCGGTCAAGTGGGTGGTGGCTTCTTCAGCACTTCTTCAAGGTGCGTCCACCAAGTGCAG 857
Oy 221 TyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAsp 240
|||||
Db 858 TACCTACCTTAGGAGCAGGCTTTCATCAAGCGCCACTTCTCCAGACAGAGATTCGAC 917
Oy 241 PheHisLysTyrIleLysArgSerMetGluAspAspPheLysValValAlaGlyIleSer 260
|||||
Db 918 TTCCACAGATCATCAAGAGGTCATGAGAGCACTTCAAGTCTGCTGGCATCAGC 977
Oy 261 LeuProLeuTrpCysValAlaIleLeuThrPheLeuAspIleAspGlyIleGlyThr 280
|||||
Db 978 CTCCCGTGTGGCTGTGGCATCTTCACTCTTGTGATATGACAGGAGTGGCACA 1037
Oy 281 LeuThrTrpIleSerPheIleProLeuValIleLeuLeuCysValGlyThrLysLeuGlu 300
|||||
Db 1038 CTCACCTGGGTTCTTTCATCTCCATCATCTCTGTGTGTTGGAACCAAGCTTAGAG 1097
Oy 301 MetIleIleMetGluMetAlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAla 320
|||||
Db 1098 ATGATCATCATGGGATGGCCCTGAGATCCAGAGCGGATCGAGCGTATCAAGGGGCA 1157
Oy 321 ProValValGluProSerAsnLysPhePheTrpPheHisArgProAspTrpValLeuPhe 340
|||||
Db 1158 CCGGTGTGAGCGCCAGCAAGATGCTTCTGTTCCACCGCCGACTGGGCTCTCTTC 1217
Oy 341 PheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValTrpThrVal 360
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Db 1218 TTCATACACCTGACGCTGTCCAGACGCTTTCATGATGGCACTTTCGTGTGACACGTG 1277
Oy 361 AlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
|||||
Db 1278 GCCACGCGCGCTTGAAGAGACTGCTTCATATGAAATCGAGGCTCAGATCATCAAGGTC 1337
Oy 381 ValLeuGlyLeuAlaLeuGluAlaPheLeuCysSerTyrIleThrPheProLeuTyrAlaLeu 400
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Db 1338 GTGCTGGGCTGGCTCTCCAGTCTGTGACAGTCACTACCTTCCCTCTACGCGCTA 1397
Oy 401 ValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThrAlaLysAla 420
|||||
Db 1398 GTCAACAGATGGATCAACATGAAAGGTCCATCTTGACAGACACACAGCCAAAGCG 1457
Oy 421 LeuThrAsnTrpArgAsnThrAlaLysGluLysLysValArgAspThrAspMetLeu 440
|||||
Db 1458 CTGACAACTGGCGGAAACAGCGCCAAAGAGAAAGAGTCCAGACCGGACATGCTG 1517
Oy 441 MetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSerProMetProSerArg 460
|||||
Db 1518 ATGCGCGAGATGATCGGCGACCAACACCGCGAGGACAGTCCCATGCTTAGCGGG 1577
Oy 461 AlaSerSerProValHisLeuLeuHisLysGlyLysMetGlyArgSerAspAspProGlnSer 480
|||||
Db 1578 GGCCTCATGCGCGGTGACCTGCTTCAAGAGGCAATGGAGCGGTGAGATGCCACAGAGC 1637
Oy 481 AlaProThrSerProArgThrMetGluAlaArgAspMetLysProValValAla 500
|||||
Db 1638 GCACCGACCTCGGCAAGAGCCATGGAGAGGCTTAGGACATGTGACCGGTTGTGGTGG 1697
Oy 501 HisProValHisArgLeuAsnProAlaAspArgTrpArgSerValSerSerAlaLeu 520
|||||
Db 1698 CATCTGTACACAGACTAAATCTGCTCAGAGCGGAGTGGGTCTTTCATCAGCCCTC 1757
Oy 521 AspAlaAspIleProSerAlaAspPheSerPheSerGlnGly 534
|||||
Db 1758 GATGCGCAATCCCGCAGACAGATTTTCTTCAAGCGGGA 1799
RESULT 7
AAF24585
ID AAF24585 standard; DNA; 1886 BP.
XX
AC AAF24585;

XX 20-APR-2001 (first entry)
XX Nucleotide sequence of the wheat M10 protein Trm103.
DE Wheat: fungal resistance: fungal pathogen; Erysiphe graminis; papillae;
KM powdery mildew; M10; cell wall apposition; transgenic plant; ss.
XX Triticum sp.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 198..1802
FT /tag= a
FT /product= "M10 protein"
XX
XX MO200078799-A2.
XX
XX 28-DEC-2000.
XX
XX 16-JUN-2000; 2000MO-EP05576.
XX
XX 18-JUN-1999; 99US-0336112.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GRS MBH.
XX
XX Salmeron JM, Welislo LJ, Strawn LJ, Kramer CM, Wang HX;
PI Vernoolt BT, Levin JZ, Helfetz PB, Patton DA, Que Q;
XX WPI: 2001-112311/12.
DR P-PSDB: AAB31252.
XX
XX Novel polynucleotide which encodes M10 protein from wheat, useful for
PT producing fungal resistant plants, in particular wheat plant -
XX
XX Claim 2; Page 97-99; 128bp; English.
PS
XX The present sequence encodes a M10 protein. M10 proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC M10 proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews). In barley, mutations at the M10
CC locus are responsible for a plant resistant phenotype. The mechanism
CC of M10 resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding M10 proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.
XX
SQ Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

Alignment Scores:
Pred. No.: 1,13e-263 Length: 1886
Score: 2680.00 Matches: 513
Percent Similarity: 98.13% Conservative: 11
Best Local Similarity: 96.07% Mismatches: 10
Query Match: 96.26% Indels: 0
DB: 22 Gaps: 0

US-09-857-896A-32 (1-534) x AAF24585 (1-1886)
QY 1 MetAlaGluAspTyrGluTyrProProAlaArgThrLeuProGluThrProSerTrpAla 20
DB 198 ATGGCAAGGACGACGGGTACCCCGGGGGGAGCGGCGGAGCGCGCTGGGCG 257
QY 21 ValAlaLeuValPheAlaValMetIleIleValSerValLeuGluGluHisAlaLeuHis 40
DB 258 GTGGCGTGTCTTCGCCGTCATGATCATCGTCCGCTCGGAGACGCGCTCCAC 317
QY 41 LysLeuGluHisTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
DB 318 AAGCTGGCGCATTTGGTTCACAGCGGACAGAGACGGCGGCGGAGCGCGAGAG 377
QY 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuLeuAlaValThrGlnAsp 80

DB 378 ATGAGCGGAGAGTATGATGCTGGTGGATTCATCTCGTGGCTCGCCGTCACGAGAC 437
QY 81 ProIleSerGlyIleCysIleSerGluLysAlaAlaSerIleMetArgProCysSerLeu 100
DB 438 CCAATCTCGGATATGATCTCCAGAAAGCGGCGGACATATGCGCCCTCAAGAGTG 497
QY 101 ProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysLysGlyLysVal 120
DB 498 GAACCGGTTCCGTCAAGAGACAGTACAGAGACTACTCGCCCAAGAGGCGAAGTG 557
QY 121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValIleValAla 140
DB 558 GCGCTATGTCACGAGGAGCGCTCACACAGCTCCACATATTCATCTTGCTAGCGGTC 617
QY 141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrp 160
DB 618 TTCATGTCACCTACAGCGATCATCATGCTCTTAAGCCGCTCAAGATGACAGATGG 677
QY 161 LysLeuTrpGluThrGluThrAlaSerLeuGluTyrGluPheAlaAsnAspProAlaArg 180
DB 678 AAGAAATGGAGACAGAAACCGCTCTTGGAATACAGATTCCGAATGATCTGGCGGG 737
QY 181 PheArgPheThrHisGlnThrSerPheValLysArgHisLeuGlyLeuSerThrPro 200
DB 738 TTCGGCTTCACGACACAGACGTCGTTGTAACCGGACCTGGCGCTGCAGACCCCC 797
QY 201 GlyIleArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLysValAsp 220
DB 798 GCGGTCAATGGGTGGTGGCTTTTCAGGCACTTTCAGTGGGTCCAGTCCACAGGTGAC 857
QY 221 TyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAsp 240
DB 858 TACCTACCTTAGGAGGAGCGCTCATCAAGCCCATTTGTCCAGAAAGAGTTTCGAC 917
QY 241 PheHisLysTyrIleLysArgSerMetGluAspPheLysValValValGlyIleSer 260
DB 918 TTCACACATGATCAAGAGGTCCATGAGAGAGACTTCAAGTCTGTTGGCATCAGC 977
QY 261 LeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThr 280
DB 978 CTCGCCCTGGGGCTGGCGATCTCACCCCTCTTGATATGACGGGATCGGACACA 1037
QY 281 LeuThrTrpLysSerPheIleProLeuValIleLeuLeuCysValGlyThrLysLeuGlu 300
DB 1038 CTCACATGGGTCTTTTATCTCTCATATCTCTTGTGTGGAAACCAAGTATGAG 1097
QY 301 MetIleIleMetGluMetAlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAla 320
DB 1098 ATGATCATATGAGGATGGCCCTGAGATCCAGAGACCGGTGCGACGTCATCAAGGGGCA 1157
QY 321 ProValValGluProSerAsnLysPhePheTrpPheHisArgProAspTrpValLeuPhe 340
DB 1158 CCGGTGGTGCAGGCCAGACAAAGTTTCTTGTTCCACCGCCGAGTGGGTCTCTTC 1217
QY 341 PheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValTrpThrVal 360
DB 1218 TTCATACACTGACGCTGTCCAGAACGCTTTCAGATGACACATTTGCTGGACAGTG 1277
QY 361 AlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
DB 1278 GCCACGCGCGGCTTGAAGAGACTGCTTCATATGAAACATGGCGTCAAGCATCAAGAGTC 1337
QY 381 ValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrIleThrPheProLeuTyrAlaLeu 400
DB 1338 GTGCTGGGCTGGCTCTCCAGATCTCTGTGAGTACATCACTTCCCTCTACGCGCTA 1397
QY 401 ValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThrAlaLysAla 420
DB 1398 CTCACACATGATGGATCAAAACATGAAGGTCCATTTGACAGACACAGCAAGCGG 1457
QY 421 LeuThrAsnTrpArgAsnThrAlaLysGluLysLysValAlaArgPheThrAspMetLeu 440

DB 1458 CTGACCAACTGGCGGACACAGGCGCAAGAGAGAGAGAGTCCGACAGCAGCATCTCTG 1517
QY 441 MetLagMettLiegYAspAlaThrProSerArgGlyThrSerProMetProSerArg 460
DB 1518 ATGGCGCAGATGATGCGGCGACGCAACCCAGCGAGGACGTCCTCCCATCTTACGCCGG 1577
QY 461 AlasSerProValHisLeuLeuHisGlyMeGlyArgSerAspAspProGlnSer 480
DB 1578 GGCTCATCGCGCGGTGACCTGCTTCAGAGGCGATGGACGCTGAGAGATCCCAAGC 1637
QY 481 AlaProThrSerProArgThrMetGluGluAlaArgAspMetTyProValValAla 500
DB 1638 GCACCGACCTCGCCAGAGCCATGGAGAGGCTTACGACATGATCCGCTGTGTGGCG 1697
QY 501 HisProValHisArgLeuAsnProAlaAspArgArgSerValSerSerSerAlaLeu 520
DB 1698 CATCTGTACACAGACTAAATCTGTGACAGCGGAGGTGCGTCTTTCATCAGCCCTC 1757
QY 521 AspAlaAspIleProSerAlaAspPheSerPheSerGlnGly 534
DB 1758 GATGCCGACATCCCAAGCGAGATTCTTCTCAGCCAGGA 1799

RESULT 8
AAV35022 standard; DNA; 1602 BP.
AAV35022:

13-OCT-1998 (first entry)

Hordeum vulgare cv. Ingrid MLO gene.

Barley; MLO; mildew; pathogen; resistance; ss.

Hordeum vulgare.

Location/Qualifiers

1..1602

/tag "a

/product "MLO protein

MO9804586-A2.

05-FEB-1998.

29-JUL-1997; 97WO-GB02046.

07-MAR-1997; 97GB-0004789.

29-JUL-1996; 96GB-0015879.

30-OCT-1996; 96GB-0022626.

(INNE-) INNES CENT INNOVATIONS LTD JOHN.

Bueschges R, Panstruga R, Schulzelefert PKJ;

WPI; 1998-159149/14.

P-PSDB; AAM59442.

New isolated MLO gene of barley - used to develop products for the production of transgenic plants which have increased pathogen resistance

Claim 2; Fig 2; 150pp; English.

The sequence is that of the MLO gene, wild-type MLO exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of MLO function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to stimulate a defence response in a plant by interaction with encoded polypeptide.

SQ Sequence 1602 BP; 336 A; 488 C; 466 G; 312 T; 0 other;

Alignment Scores:

Pred. No.: 1,25e-238 Length: 1602

Score: 2434.00 Matches: 471

Percent Similarity: 92.99% Conservative: 20

Best Local Similarity: 89.20% Mismatches: 33

Query Match: 87,43% Indels: 4

DB: 19 Gaps: 3

US-09-857-896A-32 (1-534) x AAV35022 (1-1602)

9 ProAlaArgThrLeuProGluThrProSerThrAlaValAlaLeuValPheAlaValMet 28

22 CCGGCGCGGAGCTGCCGAGAGCCGCTGTCGGCGGGGGGCTTCCGCCCATG 81

29 IleIleValSerValLeuLeuGluHisAlaLeuHisGlySerLeuGlyHisThrPheHisLys 48

82 GTGCTGTCTGCTCATGTGAGAACGGCTCCCAAGCTCGGCAATGTTGCCAGCAC 141

49 ArgHisLysAsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuVal 68

142 CGGCACAAAGAGCCCTGTGGAGGCGCTGGAGAAAGATGAAGCGGAGCTCATGCTGGTG 201

69 GlyPheIleSerLeuLeuAlaValThrGlnsPro--IleSerGlyIleGlyIle 87

202 GGCTTCATATCCCTGCTCATGTGAGAACGGCTCCCAAGCTCGGCAATGTTGCCAGCAC 261

88 SerGluLysAlaAlaSerIleMetArgProCysSerLeu--ProProGlySerValLys 106

262 FCCGAGATGCGCGCGACGTCATGTGCGCTGCAAGCGCGGACCCAGAGGCGGCAAGCCC 321

107 SerLysTrpLysAspTrpTrpLysAlaLysLysGlyLysValSerLeuMetSerThrGly 126

322 AGCAAGTACGTGACAC-----TCCCCGAGGGGCAAGGTGGCGCTCATGTCCACGGGC 375

127 SerLeuHisGlnLeuHisIlePheIlePheValLeuAlaValPheHisValThrTrpSer 146

376 AGCTTGACACGACGTCGACGCTTCATCTTCGTCGCGGCTTCATGTCACATACAC 435

147 ValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrpLysTrpLysTrpLysTrpLys 166

436 GTCATCACATAGCTCTAAGCCGCTCAAAATGAGAACATGAGAAATGGAGACAGAG 495

167 ThrAlaSerLeuGluTrpGlnPheAlaAsnAspProAlaArgPheArgPheThrHisGln 186

496 ACCACCTCTTGGAAATACCATGTCGCAATATGTCACGCTTCGCGGTTCACGACACAG 555

187 ThrSerPheValLysArgHisLeuGlyLeuSerSerThrProGlyIleLeuTrpValVal 206

556 ACGTCGTCGAGAAAGCCACCTGGGCTCTCCAGACACCCCTGGCATCGATGGGTGGTG 615

207 AlaPhePheArgGlnPhePheArgSerValThrLysValAspTrpLeuThrLeuArgAla 226

616 GCGCTTCTTCAGGCGAGTCTTCAGTCACGACCAAGGTGAGCACTGACCTTGAGGGCA 675

227 GlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLysTrpLys 246

676 GGCTTCATCAACCGCATTTGTTCGAAAGCAAGTTCATCTCCACAAAGTACATCAG 735

247 ArgSerMetLysAspAspPheLysValValValGlyLysLeuProLeuTrpCysVal 266

736 AGTTCGATGAGAGACACTTCAAGGTCTCTCGGCGCATAGCCTCCGCTGGGGGTGTG 795

267 AlaIleLeuThrLeuPheLeuAspIleAspIleIleIleIleIleIleIleIleIleIleIle 286

796 GCGATCTCTACCTCTTCTTACATCAATAGGGTGTGGCGGTCTATCTGGATTTCTTTC 835

287 IleProLeuValIleLeuLeuGlyValGlyThrHisLeuGluMetIleIleMetGluMet 306

856 ATCCCTCTCGTATCTCTTGTGTGTGAGAACCAAGCTGAGATGATCATCATGAGAGATG 915

307 AlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAlaProValValGluProSer 326

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Db 916 GCCCTGGAGATCCAGGACGGGCGCATATCAAGGGGCCCCGGTGGAGCCAGC 975
Qy 327 ASnlySPhePheTrrPheHlsArgProAspTrValLeuPhePheHlsLeuThrLeu 346
Db 976 AACAGTCTCTGCTTCACCGCCGCGGACTGGGCTCTCTTCATACACCTGACGTTG 1035
Qy 347 PheGlnAsnAlaPheGlnMetAlaHlsPheValTrpThrValAlaThrProGlnLeuLys 366
Db 1036 TTCACAGACGCGTTTCACATGCGCATTTTGTGTGACAGAGTGGCCACCGCGCTTAAG 1095
Qy 367 LysCysPheHlsMetHlsIleGlyLeuSerLysMetLysValValLeuGlyLeuAlaLeu 386
Db 1096 AAATGCTACCAACAGCAGATCGGCTGAGCATCATGAAGTGTGTGGGCTAGCTCTC 1155
Qy 387 GlnPheLeuCysSerTrpLysIleThrPheProLeuTrpAlaLeuValThrGlnMetGlySer 406
Db 1156 CAGTCTCTGACAGCTATATGACCTTCCCTCTACGCGCTGTACACACATGGGATCA 1215
Qy 407 AsnMetLysArgSerLysPheAspGlnThrAlaLysAlaLeuThrAsnTrpArgAsn 426
Db 1216 AACATGAMAGGTCATCTTCAGACAGACAGCCTCCAGCGCGCTCACCACTGGCGGAGAC 1275
Qy 427 ThrAlaLysGlnLysLysLysValArgAspThrAspMetLeuMetAlaGlnMetIleGly 446
Db 1276 ACGGCCAAGAGAAAGAAAGATCCGAGACAGCAGACATGCTGATGCTCAGATATCGGC 1335
Qy 447 AspAlaThrProSerArgGlyThrSerProMetProSerArgAlaSerSerProValHls 466
Db 1336 GACGCAACACCGAGCGGCTGCTCCGATGCCAGCGCGGCTCATACACCGCTGCAC 1395
Qy 467 LeuLeuHlsLysGlyMetGlyArgSerAspAspProGlnSerAlaProThrSerProArg 486
Db 1396 CTGCTTCACAAAGGATGGGGGCTGCGAGAGACCCCAAGCGCCCACTGCCCAAGG 1455
Qy 487 ThrMetGlnGlnAlaArgAspMetLysProValValAlaHlsProValHlsArgLeu 506
Db 1456 ACCCAGACAGAGGTAGGAGACATGTACCGGTTGTGTGGCGCACCGGCTGCACAGACTA 1515
Qy 507 AsnProAlaAspArgArgArgSerValSerSerSerSerAlaLeuAspAlaAspIleProSer 526
Db 1516 AATCTTAACAGACAGAGAGGTGCGCTGCTGCTGCGGCTGTGAAGCGGACATCCCAAGT 1575
Qy 527 AlaAspPheSerPheSerLysGly 534
Db 1576 GCAGATTTCCTTCAGCCAGGGA 1599

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RESULT 9
AAV35026 standard; cDNA; 1917 BP.

AC AAV35026;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS Hordeum vulgare.
XX
FT Key Location/Qualifiers
FT CDS 225..1826
FT /tag= a
FT /product= MLO protein
FT 1890..1895
FT /tag= b
XX
XX MO9804586-A2.
XX
XX 05-FEB-1998.
XX
XX 29-JUL-1997; 97wo-GB02046.

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XX 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
XX
XX WPI: 1998-159149/14.
DR P-PSDB; AAM59443.
XX
PT New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Disclosure: Fig 7; 150pp; English.
XX
XX The sequence is that of the MLO gene, wild-type MLO exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of MLO function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.
XX
SQ Sequence 1917 BP; 395 A; 575 C; 554 G; 393 T; 0 other;

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Alignment Scores:

Pred. No.:	6,76e-238	Length:	1917
Score:	2428.00	Matches:	470
Percent Similarity:	92.808	Conservative:	20
Best Local Similarity:	89.028	Mismatches:	34
Query Match:	87.21%	Indels:	4
DB:	19	Gaps:	3

US-09-857-896A-32 (1-534) x AAV35026 (1-1917)

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Qy 9 ProAlaArgThrLeuProGlnTrpProSerTrpAlaValAlaLeuValPheAlaMet 28
Db 246 CCGGCGCGGAGAGCTCGCGAGACCGCGTGTGGGGTGGGGTCTTCCGCCCATG 305
Qy 29 IleIleValSerValLeuLeuGlnHlsAlaLeuHlsLysLeuGlnHlsTrpPheHlsLys 48
Db 306 GTGCTCGTGTCTCGCTTCATGAGACAGCGGCTCCCAAGCTCGGCTATGTTCAGAC 365
Qy 49 ArgHlsLysAsnAlaLeuAlaGlnAlaLeuGlnLysIleLysAlaGlnLeuMetLeuVal 68
Db 366 CGGCAAGAAAGGCCCTGTGGGAGCGCTGGAGAAATGAAGCGGACCTACTGCTGGTG 425
Qy 69 GlyPheIleSerLeuLeuAlaValThrGlnAspPro---IleSerGlyIleCysIle 87
Db 426 GGCCTCAATGCCGTCTCCATCGTACAGAGACCCCATCATCCCAAGATATGACATC 485
Qy 88 SerGlnLysAlaAlaSerIleMetArgProCysSerLeu---ProProGlnSerValLys 106
Db 486 TCCGAGATGCGCGCGAGCATGATGTGGCTGTCAAGCGCGCACCGAGGGCGCAAGCCC 545
Qy 107 SerLysTrpLysAspTrpTrpCysAlaLysLysGlyLysValSerLeuMetSerThrGly 126
Db 546 AGCAAGATACGTTGACTAC-----TGCCCGAGAGGCAAGGTGGCGCTCATGTCCAGCGGC 599
Qy 127 SerLeuHlsGlnLeuHlsIlePheIlePheValLeuAlaValPheHlsValThrTrpSer 146
Db 600 AGCTTGACACGAGCGGACGCGTGAATCTTCGCTGCGGGCTTCATCATCTACATACGC 659
Qy 147 ValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrpLysLysTrpLeuThrGlu 166
Db 660 GTCATCACACATAGCTCTAAGCGCTCTCAAAATGAGAAATGAGAAATGAGAGACAG 719
Qy 167 ThrAlaSerLeuGlnTrpGlnPheAlaAsnAspProAlaArgPheArgPheThrHlsGln 186

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Db 720 ACCACCTCCTGGAATACGAGTTCCGAATATGATCTGCAGGTTCCGGTTCAACGACAG 779
Qy 187 ThrSerPheVal1LysArgHisLeuGlyLeuSerThrProGly1IleArgTyrVal1Val 206
Db 780 AGCTGCTCGTGAAGCCGCTCGCTCTCCACACCCCTGGCATCAAGATGGGCTGG 839
Qy 207 AlaPheArgGlnPhePheArgSerVal1ThrLysVal1AspTyrLeuThrLeuArg1Ala 226
Db 840 GCGTCTTCAGGAGCTTCTTCAGGTCACTACCAAGGGGAGCTACCTGACCTTGAAGGGA 899
Qy 227 GlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLysTyrIleLys 246
Db 900 GGCCTTCATCAACGCGCATTTGTCGCAAAACAGCAAGTTCGACTTCACAAAGTACATCAAG 959
Qy 247 ArgSerMetGluAspAspPheLysVal1Val1Gly1IleSerLeuProLeuTrpCysVal 266
Db 960 AGGTCGATGAGAGACGACTTCAGAGTCTGTCGCGCATCACCTCCGCGTGGGGTGG 1019
Qy 267 Ala1IleuThrLeuPheLeuAsp1IleGly1IleGly1ThrLeuThrTrp1IleSerPhe 286
Db 1020 GCGATCTCACCTCTCTCTGACATCAATGGGGTGGACGCGCTCATCTGGATTCTTTC 1079
Qy 287 1IleProLeuVal1IleLeuLeuCysVal1GlyThrLysLeuGluMet1IleMetGluMet 306
Db 1080 ATCCCTCTCGGATCCCTCTGTGTGTGGACCAAGCTGAGATGATCATCATGAGAGATG 1139
Qy 307 AlaLeuGlu1IleGlnAspArgAlaSerVal1IleLysGly1AlaProVal1Val1GluProSer 326
Db 1140 GCGCTGAGATCCAGACCGGCGGACGTCATCAAGGGGGGCGCCGCGTGGTCAAGCCCAAC 1199
Qy 327 AsnLysPhePheTrpPheHisArgProAspTrpVal1LeuPhePhe1IleHisLeuThrLeu 346
Db 1200 AACAGTCTCTTGTGTTCCACCCCGCATGCGTCCCTTCATACACCTGACAGCTGG 1259
Qy 347 PheGlnAsnAlaPheGlnMetAlaHisPheVal1TrpThrVal1AlaThrProGlyLeuLys 366
Db 1260 TTCCAAGACGGGTTTCAGATGGGCGCATTTGTGTGAGACAGTGGCCAGCCGCGCTGAAG 1319
Qy 367 LysCysPheHisMetHis1IleGlyLeuSer1IleMetLysVal1Val1LeuGlyLeuAlaLeu 386
Db 1320 AATGCTACACACGACAGATCGGGCTGACATCAAGAGTGGTGGGGGCTAGGCTTC 1379
Qy 387 GlnPheLeuCysSerTyr1IleThrPheProLeuTyrAlaLeuVal1ThrGlnMetGlySer 406
Db 1380 CAGTTCCTCTGAGCTATATGACCTTCCCTCTACGCGCTCGTCAACAGATGGGATCA 1439
Qy 407 AsnMetLysArgSer1IlePheAspGluGlnThrAlaLysAlaLeuThrAsnTrpArgAsn 426
Db 1440 AACTGAGAGGCTCATCTTCAGACGACGACGCTCAAGGGCGTCAACACTGCGGAAC 1499
Qy 427 ThrAlaLysGluLysLysLysVal1ArgAspThrAspMetLeuMetAlaGlnMet1IleGly 446
Db 1500 ACGGCCAAGGAGAAAGAAAGTCCGAGACAGGACGATGCGTATGCGTATGATCGGCG 1559
Qy 447 AspAlaThrProSerArgGlyThrSerProMetProSerArgAla1AspSerProValHis 466
Db 1560 GACGCAACACCGAGCGAGGCTGCGCCGATGCCAGCCGGGCTATATACCCGCGCAC 1619
Qy 467 LeuLeuHisLysGlyMetGlyArgSerAspAspProGlnSerAlaProThrSerProArg 486
Db 1620 CTGCTTCACAAAGGCGATGGGCGGTGCGAGCAGCCCGAGCGCGCCACTCGCCCAAG 1679
Qy 487 ThrMetGluGluAlaArgAspMetTyrProVal1Val1AlaHisProValHisArgLeu 506
Db 1680 ACCGACGAGGAGGCTAGGAGCATGTACCCGGTGTGGGGCGACCCGGTGCACACACTA 1739
Qy 507 AsnProAlaAspArgArgArgSerVal1SerSerSerAlaLeuAspAlaAsp1IleProSer 526
Db 1740 AATCTTAACGACAGAGAGAGGTCCGCGCTGCTGCGCCCTCGAAGCCGACATCCCACT 1799
Qy 527 AlaAspPheSerPheSerGlnGly 534
Db 1800 GCAGATTTTCTCTCAGCGAGGA 1823

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RESULT 10
AAV35030
AAV35030 standard: cDNA: 1635 BP.
XX
AC AAV35030:
XX
DE 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene homologue.
XX
KM Barley; MLO: mildew; pathogen; resistance: ss.
OS Hordeum vulgare.
XX
FH Key Location/Qualifiers
FT CDS 1..1635
FT /tag= A
FT /product= MLO protein homologue
XX
PM W09804586-A2.
XX
PD 05-FEB-1998.
XX
PE 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, SchulzeJelefert PMJ;
XX
DR WPI: 1998-159149/14.
XX
DR P-PSDB: AAW59445.
XX
PT New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Claim 9; Fig 11; 150pp; English.
XX
CC The sequence is that of a homologue of the MLO gene, wild-type MLO
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of MLO function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 1635 BP; 315 A; 496 C; 520 G; 304 T; 0 other:
XX
Alignment Scores:
Pred. No.: 1,02e-188 Length: 1635
Score: 1946.00 Matches: 384
Percent Similarity: 77.51% Conservative: 40
Best Local Similarity: 70.20% Mismatches: 85
Query Match: 69.90% Indels: 38
DB: 19 Gaps: 3
US-09-857-896a-32 (1-534) x AAV35030 (1-1635)
Qy 11 ArgThrLeuProGluThrProSerTrpAlaValAlaLeuValPheAlaValMetIle1Ile 30
Db 22 CGGAGCTGTGCGCACCGCGCGGTGGGTGGGTGATCTGCGCGCTATATATCTC 81
Qy 31 ValSerValLeuLeuGluHisAlaLeuHisLysLeuGlyHisTrpPheHisLysArgHis 50
Db 82 GTCTCCCTCCCATGAGACCGCGCTCCACAAAGCTGGGCGACATGCTTCACAAAGTGGCGC 141

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51 LysAsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValGlyPhe 70
 142 AAGAAGCCCTGGGGAGAGCGCTGGAGAAAGATGAGCGGAGCTCATGCTGGGGCTTC 201
 71 IleSerLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGluLys 90
 202 ATATCCCTGCTCCTCATCTCCTCAGCAGAGATCCCTCCTCAGATCTGCTCCAGAGAG 261
 91 AlaIaSerIleMetArgProCysSerLeuProGlySerValLysSerIleTyrLys 110
 262 GCCCGCCAGAAAGTGTCTCCCGTGCAGAGCTTACGACGGCGCCGGCGGTGGCAAGAGCAG 321
 111 AspTyrTyr----- 113
 322 GACAAATCACCGAGAGCTTCTGCTCCAAAGCGAGAGCCAGCCACCGCGGTTCCTG 381
 114 -----CysAlaLysLysGlyLysValSerLeuMetSerThr 125
 382 GCTGCCCCGGCCGAGTGCAGCTCTGCGCCCAACAGGCGCAAGGTGGCGCTGATGTCAAGC 441
 126 GlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaValPheHisValThrTyr 145
 442 GGAAGCATGCACCACTGCACATATTCATTCCTGCTCCCTCTCCACCTCTTGATC 501
 146 SerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTyrLysIleTyrProLthr 165
 502 AGCGTGTGCACATGACCTTAAGCGCTCTCAAAATGAGCAATGAGAACAGTGGAGTGC 561
 166 GluThrAlaSerLeuGluTyrGlnPheAlaAsnAspProAlaArgPheArgPheThrHis 185
 562 GAGACCGCTGCTGAGATCATGTCGCGAATGATCATCAGGCGGTCCGATCCAGCAC 621
 186 GlnThrSerPheValLysArgHisLeuGlyLeuSerSerThrProGlyIleArgTyrVal 205
 622 CAGACGACGTTGGTAGGCGCACCTGGCCTCTCCAGCACCCCGCGGCTGAGAGGAGTG 681
 206 ValAlaPhePheArgGlnPhePheArgSerValThrLysValAspTyrLeuThrLeuArg 225
 682 GTGGCTTCTTCAAGCATGTTCTCAGTGGTGCACCAAGGTGGAGTCACTGACCTTGAGG 741
 226 AlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLysTyrIle 245
 742 CAGGCTTTCATCAACCGCATCTCTCGCAGGCAACAGTTCACACTTCACAAATGATC 801
 246 LysArgSerMetGluAspAspPheLysValAlaValGlyIleSerLeuProLeuTyrPys 265
 802 AAGAGTGTGGAGAGACGACTTCAAGTGTGCTCCGCAATGACTCAAGCTGTGATTC 861
 266 ValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThrLeuThrTyrPheSer 285
 862 GTGGCGGTCTCATCTCTTCTTGAATTCGACGGAGATCGGCACTTCTGTGATGTGC 921
 286 PheIleProLeuValIleLeuLeuGlyValGlyThrLysLeuGluMetIleIleMetGlu 305
 922 GTGGTCTCTGTGATCTCTTGTGGGTGGACCAAGCTGGAGATGGTGCATGTGAG 981
 306 MetAlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAlaProValGluPro 325
 982 ATGGCCAGAGATCCATGACCGGAGAGCGCTCGTCAAGGGTCTCCCGCTCAGAGCC 1041
 326 SerAsnLysPhePheThrPheHisArgProAspTyrValLeuPhePheIleHisLeuThr 345
 1042 AGCAACAAGTACTTCTGTGTTCAACCGGCTGAGTGGTCTTCTTCTCAATGACCTCA 1101
 346 LeuPheGlnAsnAlaPheGlnMetAlaHisPheValTyrPheValAlaThrProGlyLeu 365
 1102 CTCTTCCAGAACCGTTTCAGATGGCTCATTTCTGTGGACATGGCCACCGCCGGCTTG 1161
 366 LysLysCysPheHisMetHisIleGlyLeuSerIleMetLysValValLeuGlyLeuAla 385
 1162 AAGAAATGCTACCAAGCAAGAAATGGCATGACATCCCAAGGTCTGCTGGGGGTACCC 1221
 386 LeuGlnPheLeuGlySerTyrIleThrPheProLeuTyrAlaLeuValThrGlnMetGly 405

1222 GCCAGATCTTGTGAGTACATACACTTCCCGCTCAAGCGCTCTGCACGAGATGGCC 1281
 406 SerAsnMetLysArgSerIlePheAspGluGlnThrAlaLysAlaLeuThrAsnTyrArg 425
 1282 TCACATGTGAAGAAAGATCTTGCAGAGAGAGGCGCAAGGCGGTGACCAACTGGCA 1341
 426 AsnThrAlaLysGluLysLysValAlaArgAspThrAspMetLeuMetAlaGlnMetIle 445
 1342 AAGATGGCCAGAGAAAGAAAGAGCCCGCAGACGGGCGCATGTGATGGCGAGATGGCC 1401
 446 GlyAspAlaThrProSerArgGlyThrSerProMetProSerArgAlaSerSerProVal 465
 1402 GCGGCGCGACGCGAGCGTCCG-----TCGTGCGCGGTG 1437
 466 HisLeuLeuHisLysGlyMetGlyArgSerAspAspProGlnSerAlaProThrSerPro 485
 1438 CACCTGTCTCCAAAGGCGGCGGCGGTGCGAGACCCAGAGCGTGGCGGCGTCCCG 1497
 486 ArgThrMetGluGluAlaArgAspMetTyrProValValAlaHisProValHisArg 505
 1498 AGGCGCGAGAAAGAGCGCGGC-----GTGCAGCATCCGCGCGCCAG 1542
 506 LeuAsnProAlaAspArgArgArgSerValSerSerSerAlaLeuAspAlaAspIlePro 525
 1543 GTACCTCTTGTGAGGAGGTGGAGTGGCGCTGTGCGCGCGCTGACATTCACATCC 1602
 526 SerAlaAspPheSerPheSer 532
 1603 GTGCAGATTTGGCTTCAGC 1623
 Db
 RESULT 11
 AAV35025
 ID AAV35025 standard; DNA; 2425 BP.
 XX
 AC AAV35025;
 XX
 DT 13-OCT-1998 (first entry)
 XX
 DE Hordeum vulgare MLO gene homologue.
 XX
 KW Barley; MLO; mildew; pathogen; resistance; ss.
 XX
 OS Hordeum vulgare.
 XX
 PN W09804586-A2.
 XX
 PD 05-FEB-1998.
 XX
 PF 29-JUL-1997; 97WO-G802046.
 XX
 PR 07-MAR-1997; 97GB-0004789.
 PR 29-JUL-1996; 96GB-0015879.
 PR 30-OCT-1996; 96GB-0022626.
 XX
 PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
 XX
 PI Bueschges R, Panstruga R, Schulzelefer PMJ;
 XX
 DR WPI; 1998-159149/14.
 XX
 PT New isolated MLO gene of barley - used to develop products for the
 PT production of transgenic plants which have increased pathogen
 PT resistance
 PS Disclosure; Fig 6; 150bp; English.
 XX
 CC The sequence is that of a homologue of the MLO gene, wild-type MLO
 CC exerts a negative regulatory function on a pathogen defence response,
 CC such that mutants exhibit a defence response in the absence of pathogen.
 CC Down-regulation or out-competition of MLO function may be used to
 CC stimulate a defence response in transgenic plants conferring increased
 CC pathogen resistance, especially resistance to powdery mildew or rust.

CC The product can also be used for identifying compounds able to
stimulate a defence response in a plant by interaction with
encoded polypeptide.

XX Sequence 2425 BP; 525 A; 692 C; 596 G; 612 T; 0 other;

Alignment Scores:

Align. No.:	1,13e-175	Length:	2425
Score:	1821.00	Matches:	426
Percent Similarity:	54.71%	Conservative:	15
Best Local Similarity:	52.85%	Mismatches:	30
Query Match:	65.41%	Indels:	339
DB:	19	Gaps:	12

US-09-857-896a-32 (1-534) x AAV35025 (1-2425)

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QY 64 GluLeuMetLeuValGlyPheIleSerLeuLeuAlaValThrGlnAspPro---Ile 82
DB 1 GAGCTCATGCTGCTGGCTTATCCCTCTCTCATGTGTCAGCAGAGACCATTGATC 60
QY 83 SerGlyIleCysIleSerGlyValAlaAlaSerIleMetArgProCysSerLeu--Pro 101
DB 61 GCCAGATATGATCTCTCGAAGATGCCGCGAGCTCATGTGCTCCGCAAGCCGCGACC 120
QY 102 ProGlySerValIleSerLeuTyrlAspTyr----- 112
DB 121 GAGGGCCGAGACCCAGCAAGTACTGCTGCTGCGCGAGGTGAGCAGCAGAGCCGG 180
QY 112 ----- 112
DB 181 ACCAGCAGCTTCAGCAGTANGAGAAATCAATACGAACTTTTCTGTTTCTCTGAT 240
QY 113 -----TyrCys-AlaIleCysGlyValSerIle 122
DB 241 TGTGCTTGGCTGTAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 122 MetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValIleuAlaValPheH 142
DB 301 CATGTCCAGGGCAGCTTGACACGCTGACGCTTCATCTTCATCTTCGCTGCTGCTGCT 360
QY 142 sValThrTyrlSerValIleIleMetAlaLeuSerArgLeuLys----- 156
DB 361 TGTACCTTACGCTGATACCATATAGCTTAAAGCGGTCAAAAGTGAGCCTTGCTTCT 420
QY 156 ----- 156
DB 421 CTCTCTCTCTTTTACGCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 157 -----MetArgThr 160
DB 481 AGTAAACTGTTCATATCTGTCTCGGCATATCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 160 PLYSLYSTRGILNTHRGILNTHRGILNTHRGILNTHRGILNTHRGILNTHRGILNTHRG 176
DB 541 GAAGAAATGGAGACAGACAGACACCTCTTGGAAATGCCATTGCCAA--TGGTCAGAGAT 599
QY 176 ----- 176
DB 600 CCCCACTGCAATCTCCCTCTCTGAAACCAACCTGATGATCATTTAAAGACGAGCG 659
QY 177 -----AspProIleArg 180
DB 660 ACGATCAGAGTACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 719
QY 180 gPheArgPheThrHisGlnThrHisSerPheValIleArgHisLeuGlyLeuSerSerThr 200
DB 720 GTTCGGGTTCAGCAGCAGCAGCAGCTGTTGTTGAAGCGCACCTGGGCTCTCCAGCACCC 779
QY 200 ogIleArgThrPylal----- 205
DB 780 TGGCATCAGATGGGT--GGTAGTTTCTTTTACCTTTTACCTGCTGATGATGTTGTGGC 838
QY 206 -----ValAlaPhePheArgGlnPhePheArgSerValThrIleValAspTyrLeuTh 223
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DB 839 TTGTGAGGTGGCTTCTTCAAGCAGTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 898
QY 223 rIleuArgAlaGlyPheIleAsn----- 230
DB 899 CTTGAGGGCAGGCTTATCAAGTACAGTACGCTCCCTCTTACGCTCCGCTATGCTGCCG 958
QY 231 -----AlaHisLeuSerHisAsnSerLysPheAspH 241
DB 959 GATGTAGACGCAAAATTTATTTGCGCAGGCGCATTTGTCCAAACAGCAATGTGACTT 1018
QY 241 eHisLysTyrlIleLysArgSerMetGluAspAspPheLysValIleValIle----- 259
DB 1019 CCACAAGTACATCAAGAGGTGATGAGAGAGACTTCAAGTGTGTGTGTGTGTGTGTGTGT 1078
QY 259 ----- 259
DB 1079 CGTTCATTCCTTCTCTGACACACACACACACACACACACACACACACACACACAC 1138
QY 259 ----- 259
DB 1139 CAGGTTCACATGATTAACAATATATGAACTTGGTCTTGTCTCTGCTTCTCTCTCA 1198
QY 260 -----SerLeuProLeuTyrCysValAlaIleLeuThr 271
DB 1199 TCATGACACATTTGGCTGTGTTTGGCAGCCTCCGCTGTGGT--GTGGGATCTCTACCC 1257
QY 271 euPheLeuAspIleAspGly----- 277
DB 1258 TCTTCTTGACATCAATGATGATGACCTTCTCTGCGGTCTCTATGCTTGTTCAGC 1317
QY 277 ----- 277
DB 1318 TAAATAAACACTTGCATTCGTCGATGATCAGCGCTCATTTTCAACATTTCTTTT 1377
QY 278 -----IleGlyThrLeuThrPylleSerPheIleProLeuVal----- 290
DB 1378 CTACTCATAGGTTGGACAGCTCATGTGATTTCTTTCATCTCTCTCTCTCTCTCTCT 1437
QY 290 ----- 290
DB 1438 ATTTCCTCATGAAACAGCAACAGCAACCACTTGTATGCAATGAAACCCACACTTAT 1497
QY 291 -----IleLeuLeuCysValGly 296
DB 1498 ATTAATCAAAATGTAATTTGCGGTGCTTCTCTCAACAGATCTTGTGTGTGGA 1557
QY 297 ThrLysLeuGlnMetIleIleMetGlnMetAlaLeuGlnIleGlnAspArgHisSerVal 316
DB 1558 ACCAAGCTGGAGATGATCATGATGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCTC 1617
QY 317 IleLysGlyAlaProValIleGlnProSerAsn-LysPhePheThrPheHisAspProAs 336
DB 1618 ATCAAGGGGGCCCCCGGTGGAGCCCGACCAACAAATTTGTGTGTGTGTGTGTGTGTGT 1677
QY 336 pTrpValLeuPhePheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPh 356
DB 1678 CTGGGCTCTCTTCTCATGACCTGACCTGTGTTCAAAGCGCTTCAAGATGGCGCATTT 1737
QY 356 eValTrpThrVal----- 360
DB 1738 TGTGTGACAGTGTGACGCCACCATGAACTTGTCACTTGAATGGGTGTCAAGGACCG 1797
QY 361 -----AlaThrProGlyLeu 366
DB 1798 AGTCCGCTGATGAACCTGCTGACGAGATTTACTGTTGTAGAGCCAGCCGCTTGA 1857
QY 366 sLysCysPheHisMetHisIleGlyLeuSerIleMetLysValIleGlnGlyLeuAlaLe 386
DB 1858 GAATGTCTACACACGACGAGATGGGCTGAGATCAAGAGGTGTGTGTGTGTGTGTGTGT 1917
QY 386 uGlnPheLeuCysSerTyrlIleThrPheProLeuTyrlAlaLeu----- 400
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Db 1918 CCAATTCTCTCGACGATATATGACCTTCCCTCTCAAGCGGCTGTCACACAGATATATA 1977
Oy 401 -----ValThrGlnMetGlySerAsnMetLysArgse 411
Db 1978 ACCGTATCATCTGTGTGCTGCTGGCTTTGTATG-CAGATGGATCAACATGAAGAGAGTTC 2036
Oy 411 rtlepaspjuginthrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLys 431
Db 2037 CATCTTCGACGAGACGAGACGCTCAAGCGCTCACCACTGGCGGAACACGCGCAAGAGAA 2096
Oy 431 sLysLysValArgAspThrAspMetLeuMetIleGlnMetIleGlyAspAlaThrProse 451
Db 2097 GAAGAAAGTCCAGACACGACGATGCTGATGATGCGGACGACGACACACCGAG 2156
Oy 451 rArgGlyThrSerProMetProSerArgAlaSerSerProValHisLeuLeuHisLysGlu 471
Db 2157 CCGAGGCTCGTCGCGCAGATGCCGACCGCGGCTCATACCCGTCGCTTCACAAAGG 2216
Oy 471 yMetGlyArgSerAspAspProGlnSerAlaProThrSerProArgThrMetGluGluAl 491
Db 2217 CATGGGCGGTCGGACGACACCCCGACGCGGCTGCTGCGCAAGAGACCGACGAGAGGC 2276
Oy 491 sArgAspMetLysProValValAlaHisProValHisArgLeuAsnProAlaAspArg 511
Db 2277 TAGGACATGTACCGGTTGTGTGGCGCACCGGTCGACAGACAAATCTTAACGACAG 2336
Oy 511 gATArgSerValSerSerSerAlaLeuAspAlaAspIleProSerAlaAspPheSerP 531
Db 2337 GAGGAGTCCGCGCTGCTGCTGCGGCTCGAAGCGGACATCCCGCAGTTCCTTTCCTT 2396
Oy 531 eSerGlnGly 534
Db 2397 CAGCCAGGGA 2406

RESULT 12
AAV35028
ID AAV35028 standard; DNA; 1611 BP.
XX
AC AAV35028;
XX
DT 13-OCT-1998 (first entry)
XX
DE Oryza sativa MLO gene homologue.
XX
KM Rice; MLO; mildew; pathogen; resistance; ss.
XX
OS Oryza sativa.
XX
XX Key Location/Qualifiers
XX FT 1..1611
XX FT CDS /product= MLO protein homologue
XX
XX WO9804586-A2.
XX
PD 05-FEB-1998.
XX
PE 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
XX (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefer PKJ;
XX
XX WPI; 1998-159149/14.
XX
XX DR P-PSDB; AAW59444.
XX
XX PT New isolated MLO gene of barley - used to develop products for the
XX PT production of transgenic plants which have increased pathogen
XX PT resistance
```

```
XX
PS Claim 6; Fig 10; 150pp; English.
XX
XX The sequence is that of a homologue of the MLO gene, wild-type MLO
XX CC exerts a negative regulatory function on a pathogen defence response,
XX CC such that mutants exhibit a defence response in the absence of pathogen.
XX CC down-regulation or out-competition of MLO function may be used to
XX CC stimulate a defence response in transgenic plants conferring increased
XX CC pathogen resistance, especially resistance to powdery mildew or rust.
XX CC The product can also be used for identifying compounds able to
XX CC stimulate a defence response in a plant by interaction with
XX CC encoded polypeptide.
XX
SQ Sequence 1611 BP; 348 A; 450 C; 450 G; 363 T; 0 other:
Alignment Scores:
Pred. No.: 2,08e-167 Length: 1611
Score: 1737.50 Matches: 356
Percent Similarity: 76.34% Conserved: 57
Best Local Similarity: 65.80% Mismatches: 95
Query Match: 62.41% Indels: 33
DB: 19 Gaps: 11
US-09-857-896A-32 (1-534) x AAV35028 (1-1611)
Oy 10 AlaArgThrLeuProGlnThrProSerTrpAlaValAlaLeuValPheAlaValMetIle 29
Db 22 TGGCGGAGTGGCGGAGAGCGGAGCGGAGCGGCGGCTGCTGCGGCTGCTGCGGCTGCTG 81
Oy 30 IleValSerValLeuLeuGlnHisAlaLeuHisLysLeuGlnHisTrpPheHisLysArg 49
Db 82 CTGCTCTCGCGCGCATGGAGACGCGGCTCCACCAACCTCAGC-----CATAAAC 132
Oy 50 HisLysAsnAlaLeuAlaGlnAlaLeuGlnLysIleLysAlaGlnLeuMetLeuValGly 69
Db 133 ACCGCAAGATTCATATTTCTTGTGCTCATCTGCACTGCAAGCTGATGATGCTGGG 192
Oy 70 PheIleSerLeuLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGlu 89
Db 193 TTCATATCCCGCTCTCCACCGTGGCAGACGCGGCCCATTCCAAAATTCGATCCCAAG 252
Oy 90 LysAlaIleSerIleMetIleArgProCysSerLeuProProIleSerValLysSerLysTr 109
Db 253 TCGGCTGCCAATCTTGTTCCTGCGTGCAGGACGCCAAGATCCCAAGAGAGCA 312
Oy 110 LysAsp-----TyrTyrCysAlaLys---Lys 117
Db 313 GCAAGTGTGCGCGGCTCTTGGCCGCGCGCGCGGAGCATGCTCGAAATTCGAT 372
Oy 118 GlyLysValSerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheVal 137
Db 373 GCGAAGGTGGCGGTGATGTCGCAAGAGCATGCGACGTCGACATTTTCATCTTCGTG 432
Oy 138 LeuAlaValPheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMet 157
Db 433 CTCGCCGTGTCATGTACTACTACATCATCATCATCGATGCGGTAGGCGCCTCAAAATG 492
Oy 158 ArgThrTrpLysLysTrpGlnThrGlnThrLysSerLeuGlnLysGlnThrGlnPheIleAsn 177
Db 493 AAGAAATGGAAGAGTGGAGTGCACAGACCAACTCATGTGAGATAGTTCGCAATCGAT 552
Oy 178 ProAlaArgPheArgPheThrHisGlnThrSerPheValLysArgHisLeuGly---Leu 196
Db 553 CTTTCAGATTCAGGTTCACCGCATCAGACGTCGTTCTGTAAGCGGCGATCGGATCATTC 612
Oy 197 SerSerThrProGlyIleArgTrpValValAlaPheArgGlnPhePheSerVal 216
Db 613 TCAAGCACCCCTGGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 672
Oy 217 ThrLysValAspTyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSerHisAsn 236
Db 673 ACCAAGGTGACTACTACATGCGGAGGAGGCTTCATCAATGCGCATTTGCGCAGAAAT 732
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OY 237 SerLysPheAspPheHisLysTyrIleLysArgSerMetGluAspPheLysValVal 256
DB 733 AGCAAGTTCCACTTCCAAATACATCAAGAGGCTTTTGGGACACACTTCAAACTTCTC 792
OY 257 ValGlyLeuSerLeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAsp 276
DB 793 GTTGGCATACAGCTCCCTCTGTGTTGGTGGATGCTTGTACTCTCTCGATATCCAC 852
OY 277 GlyIleGlyThrLeuThrTrpIleSerPheIleProLeuValIleLeuLeuCysValGly 296
DB 853 GGTCTGGCACACTTATTTGGATCTTTTGTCTCTCTCAATCGTCTGTGTAGTGGG 912
OY 297 ThrLysLeuGluMetIleIleMetGluMetAlaLeuGluIleGluInnSparGlyAspVal 316
DB 913 ACCAAGCTAGAGATGATGATCATGGATGGCCCAAGATACAGACAGGCGCACTGTG 972
OY 317 IleLysGlyAlaProValValGluProSerAsnLysPheThrPheHisArgProAsp 336
DB 973 ATCCAGGAGACCTATGTTGTTGACCAAGCAACAAAGTACTTGTGTTCAACCGCTGTAC 1032
OY 337 TrpValLeuPhePheIleHisLeuThrLeuPheGluInnSnaIaPheGluMetAlaHisPhe 356
DB 1033 TGGGCTGTGTTTTCATACACCTGACACTTTCATACACCATTTTCAGATGGCGCATTTTC 1092
OY 357 ValTrpThrValAlaThrProGlyLeuLysCysPheHisMetHisIleGlyLeuSer 376
DB 1093 GATGAGACTATGGCAACCTGTGTGAGAAATGCTTCCATGAAATATTTGGCTGAC 1152
OY 377 IleMetLysValValLeuGlyLeuAlaLeuGluInnSnaIaPheLysSerTyrIleThrPhePro 396
DB 1153 ATCGTGCAAGCTATGTTGGGGATCTCTCTCAGGTGATGACGATACATCACTCCCG 1212
OY 397 LeuTyrAlaLeuValThrGluMetGlySerAsnMetLysArgSerIlePheAspGluInn 416
DB 1213 CTCTACGGCTCTGTCACACAGATGGATGCAACATGAAGAAGACATTTTCAGAGACAA 1272
OY 417 ThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLysValArgAsp 436
DB 1273 AGGATGAAGGCGCTGATGAACTGGAGGAAGAGCGGATGCGAAGAAAGGTCCGGGAC 1332
OY 437 ThrAspMetLeuMetAlaGluMetIleGlyAsp--AlaThrProSerArgGlyThrSer 455
DB 1333 GCGGACGGCTTCCGTGGCGGAGATGACGTCGACCTTCGGGACCGCGGGG----- 1380
OY 456 ProMetProSerArgAlaSerSerProValHisLeuLeuHisLysGlyMetGlyArgSer 475
DB 1381 -----TCGAGCCGGCTCCGCGCGGTCGACCTGTG---CAGGTCAACAGGCGGGTTC 1431
OY 476 AspAspProGluInnSerAlaProThr-----SerProArgThrMetGluInnAlaArgAsp 493
DB 1432 GGAGCGCCGCGGACCCCAATCACGCGTGGCTCACACCGGACCGGAGAG-----GAC 1485
OY 494 MetTyrProValValAlaHisProValHisArgLeu-----AsnProAlaAspArg 511
DB 1486 ATGTACCCGGTGGCGGCGGCGCTGCGCTCCAGCTGCTAGACGACCCCGGACAGG 1545
OY 512 ArgArgSerValSerSerSerAlaLeuAspAlaAspIleProSerAlaAspPheSerPhe 531
DB 1546 AGGTGATGGCATCTCTGTG-----GCCGACATCGCCGATTTCTGATTTTCTCTTC 1596
OY 532 Ser 532
DB 1597 AGC 1599

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RESULT 13

AAV35029

ID AAV35029 standard; DNA; 4105 BP.

AC AAV35029;

DT 13-OCT-1998 (first entry)

DE Hordeum vulgare MLO gene homologue.

```

XX XX Barley; MLO; mildew; pathogen; resistance; ss.
KW KW
OS Hordeum vulgare.
XX MO9804586-A2.
XX PN
XX PD 05-FEB-1998.
XX PF 29-JUL-1997; 97WO-GB02046.
XX PR 07-MAR-1997; 97GB-0004789.
XX PR 29-JUL-1996; 96GB-0015879.
XX PR 30-OCT-1996; 96GB-0022626.
XX PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX PI Bueschges R, Panstruga R, SchulzeJelefert PMJ;
XX DR WPI; 1998-159149/14.
XX PT New isolated MLO gene of barley - used to develop products for the
XX PT production of transgenic plants which have increased pathogen
XX PT resistance
XX PS Disclosure: Fig 9; 150pp; English.
XX CC The sequence is that of a homologue of the MLO gene, wild-type MLO
XX CC exerts a negative regulatory function on a pathogen defence response,
XX CC such that mutants exhibit a defence response in the absence of pathogen.
XX CC Down-regulation or out-competition of MLO function may be used to
XX CC stimulate a defence response in transgenic plants conferring increased
XX CC pathogen resistance, especially resistance to powdery mildew or rust.
XX CC The product can also be used for identifying compounds able to
XX CC stimulate a defence response in a plant by interaction with
XX CC encoded polypeptide.
XX SO Sequence 4105 BP; 941 A; 1176 C; 1065 G; 923 T; 0 other.

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Alignment Scores:

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Pred. No.: 3,1e-146 Length: 4105
Score: 1536.50 Matches: 383
Percent Similarity: 42.45% Conservative: 39
Best Local Similarity: 38.53% Mismatches: 87
Query Match: 55.19% Indels: 489
DB: Gaps: 11

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US-09-857-896A-32 (1-534) x AAV35029 (1-4105)

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OY 11 ArgThrLeuProGluThrProSerTrpAlaValAlaLeuValPheAlaValMetIleIle 30
DB 783 CGGAGCTGTGCGACACCGACGACGCTGGCGGTGCTGTGCGCGCTCATGATATCTC 842
OY 31 ValSerValLeuLeuGluHisAlaLeuHisLysLeuGlyHis----- 44
DB 843 GTCTCCGTCCGATGAGACAGCGCTCCACAACTGTGGCCAGTACGTCGTGGTTCA 902
OY 44 ----- 44
DB 903 CTATGTCTTAACGTGTTTGTGATGTTTTCGGGCGTGTGTGTAACCTGCATGAGAGTGTGA 962
OY 44 ----- 44
DB 963 TGAGCCCAAAAGTTCCTCCCGGACCCACTTTTGGCTGTTGTGATGGGTATGGCTGA 1022
OY 44 ----- 44
DB 1023 GGAGAGCATCATCACTGATGCAAAAAGGCGCTCAGATAGCTAGAGCCAGCACCCCG 1082
OY 44 ----- 44
DB 1083 CAGAGGAGCTGAGGCGAGTATATGCTGAGGCCATGACACCTGCGCCCGTGGCCGCTG 1142

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DB 3299 TCGTCTGGGGGTAGCCGCCAGATCTTGTGACGTACATCACCTTCCGCTCTACGCCG 3358
QY 400 euval1thGlmctGlySerasmMetLysArgSerTlIerheasPgluGlnThralaLysA 420
DB 3359 TCGTACCCAGATGGCTCCACATCAAGAGATCTTTCGACGAGCAGCGCCCAAG 3418
QY 420 1aLeuThraNTPArgAsnThraLysGluLysLysValaTargAspThrAspMetL 440
DB 3419 CGCTGACCAACTGGCCGAAAGATGGCCAGAGAAAGAAAGAGCCCGGACGCGCCATGC 3478
QY 440 eumetalaGlmMetIleGlyAspAlaThrProSerArgGlyThrSerPrometProserA 460
DB 3479 TCGATGGCCAGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3519
QY 460 rgaLaserSerProvalInHisLeuLeuInHisLysGlyMetGlyArgSerAspAspProGlns 480
DB 3520 -----TCGTGCGCGGTCCACCTGTCTCCAAAGCGCGGCGGCGGCGGCGGCGGCGG 3574
QY 480 erAlaProThrSerProArgThrMetGluGluAlaAlaArgAspMetTyProValValaL 500
DB 3575 GCGTCCGCGCGCTCCCGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3619
QY 500 1aHisProValInHisArgLeuAsnProAlaAspArgArgSerValSerSerSerAlaL 520
DB 3620 AGCATCCGCGCGCGCAAGTACTCTTGTGACGGGTGAGGTGCGGCTGTGCGCGCGCG 3679
QY 520 euAspAlaAspIleProSerAlaAspPheserPheser 532
DB 3680 TCGACGCTCACATCCCGGTGCAGATTGCTTGCCTCAGC 3717
RESULT 14
AAZ30413
ID AAZ30413 standard; DNA; 1935 BP.
XX
AC AAZ30413;
XX
DT 21-DEC-1999 (first entry)
XX
DE Arabidopsis thaliana M10 fungal resistance gene CIB10295.
XX
KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KM papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
XX M10; Erysiphe graminis; powdery mildew; ss.
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 79..1810
FT FT /*tag= a
FT FT /product= "M10 fungal resistance protein"
XX
PN MO9947552-A2.
XX
PD 23-SEP-1999.
XX
XX 17-MAR-1999; 99MO-EP01779.
PF
XX 17-MAR-1998; 98US-0042763.
PR
PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
XX
XX Salmeron JM, Welsio LJ, Strawn LJ, Kramer CM;
PT
DR MPI; 1999-571820/48.
XX
XX P-PSDB; AAY26970.
XX
XX New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
XX Claim 3; Page 78-81; 102pp; English.
XX
XX This sequence represents the coding region for the Arabidopsis thaliana

CC fungal resistance gene CIB10295. The M10 protein confers resistance to
CC fungal pathogens by stimulating the formation of large cell wall
CC appositions, designated papillae, at the contact site with the fungal
CC pathogen. These papillae mainly contain callose, but also contain
CC carbohydrate, phenols and proteins and are used to prevent penetration
CC of the fungal hyphae into the plant. The new M10 sequences are used to
CC generate transgenic plants resistant to fungal pathogens, especially
CC Erysiphe graminis (powdery mildew).
XX

SQ Sequence 1935 BP; 576 A; 382 C; 398 G; 579 T; 0 other;

Alignment Scores:
Pred. No.: 3.78e-120 Length: 1935
Score: 1276.50 Matches: 251
Percent Similarity: 63.62% Conservative: 76
Best Local Similarity: 48.83% Mismatches: 142
Query Match: 45.85% Indels: 45
DB: Gaps: 4

US-09-857-896a-32 (1-534) x AAZ30413 (1-1935)

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DB 110 CGGACTTTAGAGGAGACCTTACGCGGAGTTGCTGTGCTTCTTCTTCTTCTTCTTCTTCTT 169
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QY 51 LysAsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValaGlyPhe 70
DB 230 AAGCAGGCTCTTTTGAAGCTTTGAAGAGCTTTGAAGAGCTTTATCTGTGTGGGTTTC 289
QY 71 IleSerLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGlyLys 90
DB 290 ATATGACTTACTACTACATTTGACAAACCAATCTCAAAATGTGCATGTCCAGAA 349
QY 91 AlaAlaSerIleMetArgProCysSerLeuProProGlySerValLysSerLysTyLys 110
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QY 111 AspTyr----- 112
DB 410 GACGCGGAAAGAAAGATGATGAGATGAGATTAACCCGCTGGAACCTTCTTGTGAG 469
QY 113 -----TyrCysAla 115
DB 470 TTACCTGATCTTATATCCATGAAAGAGTTTGACCAACGCTATGACAAATGTGCA 529
QY 116 LysLysGlyLysValSerLeuMetSerThrGlySerLeuInHisIlePheIle 135
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DB 590 TTCTGCTCGCGGTGTGTATGTGTGTATGCTGCAATGTGTACTTATGCTTTTGGAAAGATC 649
QY 156 LysMetArgThrTrpLysLysTrpGluThrGluThrAlaSerLeuGluInHisIlePheAla 175
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Oy 373 IleGlyLeuSerIleMetLysValValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyr 392
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Oy 433 LysValArgAspThrAspMetLeuMetIleGlyAspAlaThrProSerArg 452
Db 1490 AAA-----CACGGAAGACACTCGGATCCATATCACCTTCTCT 1528
Oy 453 GlyThrSerProMetProSerArgAlaSerSerProValHisLeuLeuHisLysGlyMet 472
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Oy 473 GlyArgSerAspAspProGlnSerAlaProThrSerProArg 486
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Db 1589 AACCGAGCGTTGAAAATTAACCAAGTCTCCTTCCTAGA 1630

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 15:46:08 ; Search time 56 Seconds

(without alignments)
2924.382 Million cell updates/sec

Title: US-09-857-896A-32

Perfect score: 2784
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Ygapop 10.0 , Ygapext 0.5
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cgn2_6/p1odata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1201	43.1	1851	4	US-09-183-959-9
2	902	32.4	1725	4	US-09-183-959-1
3	798	28.7	1869	4	US-09-350-266-1
4	798	28.7	1869	4	US-09-558-678-1
5	745.5	26.8	1040	4	US-09-183-958-11
6	736	26.4	1831	4	US-09-183-958-11
7	580.5	20.9	538	4	US-09-183-959-13
8	422	15.2	705	4	US-09-183-959-17
9	394.5	14.2	750	4	US-09-183-959-18
10	300	10.8	597	4	US-09-183-959-3
11	138.5	5.0	472	4	US-09-183-959-5
12	96.5	3.5	6315	2	US-08-808-793-2

13	96.5	3.5	6315	3	US-08-772-512A-2	Sequence 2, Appl1
14	96.5	3.5	6318	2	US-08-808-793-1	Sequence 1, Appl1
15	96.5	3.5	6318	3	US-08-772-512A-1	Sequence 1, Appl1
16	94.5	3.4	11721	4	US-09-026-039-3	Sequence 3, Appl1
17	94.5	3.4	11721	4	US-09-026-039-3	Sequence 3, Appl1
18	94	3.4	8838	4	US-09-417-882-1	Sequence 1, Appl1
19	93	3.3	80161	3	US-09-036-987A-1	Sequence 1, Appl1
20	93	3.3	80161	4	US-09-370-700-1	Sequence 1, Appl1
21	92	3.3	1135	4	US-09-074-879-9	Sequence 1, Appl1
22	92	3.3	7833	1	US-08-323-873A-1	Sequence 9, Appl1
23	92	3.3	7833	1	US-08-468-057A-9	Sequence 9, Appl1
24	91.5	3.3	6725	3	US-08-949-386-36	Sequence 36, Appl1
25	91.5	3.3	6725	3	US-08-450-562-16	Sequence 36, Appl1
26	91.5	3.3	6725	4	US-08-984-709A-36	Sequence 36, Appl1
27	91.5	3.3	6725	4	US-08-450-272-16	Sequence 36, Appl1
28	91	3.3	5975	1	US-08-404-354B-1	Sequence 36, Appl1
29	91	3.3	5975	1	US-08-314-083B-1	Sequence 1, Appl1
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34	90	3.2	28804	3	US-09-096-867-2	Sequence 2, Appl1
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37	89	3.2	4550	4	US-09-463-136-1	Sequence 1, Appl1
38	89	3.2	5659	4	US-09-221-017B-440	Sequence 1, Appl1
39	89	3.2	5659	6	5386025-5	Sequence 440, App
40	89	3.2	5975	1	US-08-336-257A-3	Sequence 3, Appl1
41	88	3.2	2762	1	US-08-198-446B-12	Sequence 12, Appl1
42	88	3.2	2762	2	US-08-870-693-12	Sequence 12, Appl1
43	88	3.2	5904	1	US-08-455-543A-3	Sequence 3, Appl1
44	88	3.2	5904	2	US-08-193-078B-3	Sequence 3, Appl1
45	88	3.2	5904	2	US-08-223-305C-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-183-959-9
; Sequence 9, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BR-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: NO
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 9
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-9

Alignment Scores:

Pred. No.: 6.59e-131
Score: 1201.00
Percent Similarity: 63.29%
Best Local Similarity: 47.82%
Query Match: 43.14%
DB: 4
Gaps: 5

US-09-857-896A-32 (1-534) x US-09-183-959-9 (1-1851)

OY 10 AAlarGhrhrleuProcluthrProserTrpAlaValAlaLeuValpheaAlaValMetlle 29
DB 108 TCGCGGAGCTGTGACCGACGCGCATGCGGCTGCGCTGCGCGCTGATCTCG 167

Oy	333	HisAgrpProAspTrpValLeuPhePheHisLeuThrLeuPheHisAsnAlaPheGln	352
		
Dd	1248	GCACGCCCCACCTTCGCTTCCTCCATCCACTTACCCTCTTCCAGATGGCTCCAG	130
Oy	353	MetaLHisPheValTrpPhrValAlaThrProGlyLeuLysCysPheHisMetHis	372
		
Dd	1308	ATCATCTCACTTCCTCGTACCTGTGTGATGATGATGACGGCAGGAGCTGCTTCCACATC	136
Oy	373	IllegIleuSerIleMetLysValValLeuGlyLeuAlaAlaGlnPheLeuLysSerTyr	392
		
Dd	1368	GAAAGCTTCGCTTTTGCACGACACTCGCTTGGCTGGCTGTTCACAGTCTGTGCAGTAC	142
Oy	393	IleThrPheProIleuTyrAlaLeuValThrGlnMetGlySerAsnMetLysArgSerIle	412
		
Dd	1428	GTGACGCTCCCGCTGTACACCGCTGCTCTCCCAATGGGCTCCACACAAAGAGATCCATC	148
Oy	413	PheAspGluGlnThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLys	432
		
Dd	1488	TTTCAGACAGACAGACTTCCAAAGCGCTCAAGAACTGGCGGCGGCGCAAGAAAGAGCT	154
Oy	433	LysValAlaArgAspThrAspMetLeuMetIleGlyAspAlaThrProSerArg	452
		
Dd	1548	CCCAACGGCGGC-----TCCAAACACGGCGGTGTGGCTCCCAACGCGCC	159
Oy	453	GlyThrSerPro	456
Dd	1593	GCGCGACGCCCC	1604
RESULT 2			
	US-09-183-959-1		
	/ Sequence 1, Application US/09183959		
	/ Patent No. 6303332		
	/ GENERAL INFORMATION:		
	/ APPLICANT: Cahoon, Rebecca E.		
	/ APPLICANT: Miao, Guo-Hua		
	/ APPLICANT: Rafalski, J. Antoni		
	/ APPLICANT: Tarzaniro, Grazelana		
	/ TITLE OF INVENTION: CORN GDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE		
	/ FILE REFERENCE: BB-1125		
	/ CURRENT APPLICATION NUMBER: US/09/183,959		
	/ CURRENT FILING DATE: 1998-11-02		
	/ EARLIER APPLICATION NUMBER: 60/064,493		
	/ EARLIER FILING DATE: NO. 6303332member 5, 1997		
	/ NUMBER OF SEQ ID NOS: 20		
	/ SOFTWARE: Microsoft Windows 95		
	/ SEQ ID NO 1		
	/ LENGTH: 1725		
	/ TYPE: DNA		
	/ ORGANISM: Zea mays		
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Dd	81	CTCTCTGTGCTGTGCGCGCGAGGATGCTCTCCACTACCTGCGCAGAGAGCTCAAGAGGAG	140
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Dd	141	ATCCAAAGACCGCGCTTTCGAGGCGCTGCTCAAGTCAAGAAAGAGATTGATGCTCTGGGG	200

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Qy 109 TyrLysAspTyr-Tyr- 113
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Qy 128 LeuHisGlnLeuHisIlePheIlePheValIleValPheHisValThrTyrSerVal 147
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Qy 148 IleIleMetAlaLeuSerArgLeuLysMetArgThrTyrLysTyrPgluThrGluThr 167
Db 501 ACACTATGCTTTTGTAGGAGTGACACATACACCAATGGAACAGTGGAGCAAT- 554
Qy 168 AlaSerLeuGluTyrGlnPheAlaAsnAspProAlaArgPheArgPheThrHisGlnThr 187
Db 555 ---GGAATTAATAAAGAGCTCCGGAATGGCGCTGAAGGTAAACCAATGATACATCAT 611
Qy 188 SerPheValLysArgHis-----LeuGlyLeuSerSerThrProGlyIleArgTyr 204
Db 612 GAATTTATCAAGAAAGCTTTTAAAGGTATGCGCAAGATTCATATAT- 668
Qy 205 ValValAlaPhePheArgGlnPhePheArgSerValThrLysValAspTyrLeuThr 224
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Qy 265 CysValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThrLeuThrTyrPle 284
Db 849 GTCTTGTGATATATTTCTGTCTGTAATGTAAGGCTGACACATACTTTTGGATT 908
Qy 285 SerPheIleProLeuValIleLeuLysCysValGlyThrLysLeuGluMetIleIleMet 304
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Qy 305 GluMetAlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAlaProValGlu 324
Db 969 CAGCTAGCCCATGATGATGCTGACAGACACAGCGGCTGAGGAGATGATGATCAAAA 1028
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RESULT 3
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; Sequence 1, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance
; FILE REFERENCE: 5718-42A - M103
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: M103
US-09-350-268-1

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Score: 798.00
Percent Similarity: 52.39%
Best Local Similarity: 35.18%
Query Match: 28,668
DB: 4
Gaps: 11

US-09-857-896a-32 (1-534) x US-09-350-268-1 (1-1869)
Qy 12 ThrLeuProGluThrProSerThrPalaValAlaLeuValPheAlaValMetIleIleVal 31
Db 99 ACGCGAGAGACAGCGCTACGTGATCGTGGCGTCCGTGCTCCGTCATCCTCTCATC 158
Qy 32 SerValLeuLeuGluHisAlaLeuHisLysLeuGlyHisThrPheHisLysArgHisLys 51
Db 159 TCTCTTCCTTCCTGAGCGCGCGCTCCACACCTCCGCAAGGCACTGAGCGCGCGAGAG 218
Qy 52 AsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValGlyPheIle 71
Db 219 ---ACCGTACAGAGCGCGCTGAACCTCAAGAAAGACTCATCTCTGGGCTTCGTC 275
Qy 72 SerLeuLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGluLysAla 91
Db 276 TCGGCTCCTCTGCTGCTCCAGACTTGTATACAGAAATCTGATTCACACAGCCTTC 335
Qy 92 AlaSerIleMetArgProCysSerLeuProProGlySerValLysSerLysTyr----- 109
Db 336 ATGGACACATGATGCGCGTGGGGGTGCGAGCCCAACCCCTGGGCTATACGGTGC 395
Qy 109 ----- 109
Db 396 TCTCTCTCTCTCTCTCCCGGCTGCGTGGCGGAGAGATGCTCAAGCGCGCGG 455
Qy 110 ---LysAspTyrTyrCysAlaLysLysGlyLysValSerLeuMetSerThyGlySerLeu 128
Db 456 GCACCTTTCGGGACGTCTCAAGCAAGGAAAGATCCCGTGTATCATCTGACGCGCTTG 515

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QY 129 HisGlnLeuHisIlePheIlePheValLeuAlaValPheHisValThrTyrSerValIle 148
Db 516 GAGCAGGTACACATTTCATCTTCCTGACGTATCCAGCAAGACGCTTCACGGCGCC 575
QY 149 IleMetAlaLeuSerArgLeuLysMetArgThrTyrLysTyrPglLysThrAla 168
Db 576 ACCGCTCCTCGGAGCTTTCGACATGCGATATGATGACACTGGAGAAC----- 626
QY 169 SerLeuGluTyrGlnPhePheAlaAsnProAlaArgPheArgPheThrHisGlnThrSer 188
Db 627 ACCATTACAGCAAGAGCGCAGCTGCTGCTCCAAAGATGATCCCGCTGCCAGAAATCAGG 686
QY 189 PheValLys--ArgHisLeuGlyLeuSerSerThrProGly--IleArgTyrValVal 206
Db 687 TTCATCCAGGACCGGTATAGGGGTACGAGAAGCGCGCGGTATATATGCGCTGCT 746
QY 207 AlaPhePheArgGlnPhePheArgSerValThrLysValAspTyrLeuThrLeuArgAla 226
Db 747 TCTTCTTCAAAAGTCTTCAGCATCAGTCCAAACGACGACTGCGATGCGATGAGACCTC 806
QY 227 GlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLysTyrIleLys 246
Db 807 GGTTCGTCATGAGCAGCACTTTAGGGGCGACCCCAAGTTCACATTTTACGACTACATGATC 866
QY 247 ArgSerMetGluAspAspPheLysValValValGlyIleSerLeuProLeuTyrPysVal 266
Db 867 AAGCTCTCGAAGAAAGATTTCAGACGAGTATGATATAAATGATATACGAGATTTT 926
QY 267 AlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThrLeuThrTyrIleSerPhe 286
Db 927 GTGATGATCTTCTGCTGCTCAATGTCACCGGGTGGCAGCTTCTTCTGATCTCATTA 986
QY 287 IleProLeuValIleLeuLeuCysValGlyThrLysLeuGluMetIleIleMetGluMet 306
Db 987 GTTCCACTGGCTGCTGCTGCTGATGGGAGCAGATCGGAGCATCATTAACAGCTG 1046
QY 307 AlaLeuGluIleGlnAspArg-----AlaSerValIleLysGlyAlaProValValGlu 324
Db 1047 GCGTACGAGGTGGCTCGAAGACGCGCGGGGCAAGGCGAAGGGGCGATCGGGGAGCC 1106
QY 325 ProSerAsnLysPhePheThrPheHisArgProAspTyrValLeuPhePheIleHisLeu 344
Db 1107 CCTGCGAGCAGCTGTTCTGTTCCGACGCCAGCGGTGGTGTGCTGATCATCCACTTC 1166
QY 345 ThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValThrPyrValAlaThrProGly 364
Db 1167 ATCTGTTCAGAAAGCGCTTCGAGTTCGCGTATTTCTTCTGACACTGGGAGTTCGCG 1226
QY 365 LeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysValValLeuGlyLeu 384
Db 1227 GCCAATCTCGTCAATGACAGTCTAGGATACAGCTCTCGCAATCAATCATATCCGTC 1286
QY 385 AlaLeuGlnPheLeuCysSerTyrIleThrPheProLeuTyrAlaLeuValThrGlnMet 404
Db 1287 GTCTCCAGGTGCTCTGACATACACACATCCGCTCTAGGCAATCGTGTCCATATG 1346
QY 405 GlySerAsnMetLysArgSerIlePheAspGluGlnThrAlaLysAlaLeuThrAsnTyr 424
Db 1347 GGGAGTCTGTTCAAGAGCGCTGTGTTGTTGTTGAGCAGCAGTGGCGCAATCTCAGAGGTTG 1406
QY 425 ArgAsnThrAlaLysGluLysLysValArgAspThrAspMetLeuMetAlaGlnMet 444
Db 1407 GCCAGAGGCGCCGAGGCGGTGGG---AGATCTGCCAGGGGTGTGAGCGCAATTGC 1463
QY 445 IleGly---AspAlaThrProSerArgGlyThrSerProMetProSerArgAlaSerSer 463
Db 1464 CTGGGTAGCCGGCGCGCGGAGCGGGCTGG-----GAAGGCGCGCGC 1508
QY 464 ProValHisLeuHisLysGlyMetGlyArgSerAspAspProGlnInsValaProThr 483
Db 1509 GCGTGGAGATTGATT-----GCCGGGAGGCGGACCGCCCAACTCAGCAGCCTCGG 1559
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QY 484 Ser-----ProArgThrMet 488
Db 1560 AGCATCTCCTCTGAGTTCTGTCTAGTTTCTGAAGAAGATCGAAAGCGCGCAATCTG 1619
QY 489 GluGluAla 491
Db 1620 CAGCAGCGC 1628

RESULT 4
US-09-558-679-1
; Sequence 1, Application US/09558679
; Patent No. 6403768
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance
; FILE REFERENCE: 5718-42A-- M103
; CURRENT APPLICATION NUMBER: US/09/558,679
; PRIORITY FILING DATE: 2000-04-26
; PRIORITY FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; OTHER INFORMATION: M103
US-09-558-679-1

Alignment Scores:
Pred. No.: 1.63e-83 Length: 1869
Score: 798.00 Matches: 184
Percent Similarity: 52.39% Conservative: 90
Best Local Similarity: 35.18% Mismatches: 193
Query Match: 28.66% Indels: 56
DB: Gaps: 11

US-09-857-896a-32 (1-534) x US-09-558-679-1 (1-1869)
QY 12 ThrLeuProGluThrProSerTyrPheAlaValAlaLeuValPheAlaValMetIleLeuAl 31
Db 99 ACGGTGAGGAGCAGCGCTGCTAAAGCTCAAGAAAGCTCATCTCTGTGGCTGCTCATC 158
QY 32 SerValLeuLeuGluHisAlaLeuHisLysLeuGlyHisTyrPheHisLysArgHisLys 51
Db 159 TCTCTGCTCTGCGAGCGCGCGCTCCACACCTCGGCAAGGACCTGGAGCGCGGAGAG 218
QY 52 AsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValGlyPheIle 71
Db 219 ---ACCTGTACAGAGCGCTGCTAAAGCTCAAGAAAGCTCATCTCTGTGGCTGCTGC 275
QY 72 SerLeuLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGlyLysAla 91
Db 276 TCGTGTCTCTCTGCTCTCCAGGACTGTATACAGAAAGTCTGATGAGACAGCAGCTC 335
QY 92 AlaSerIleMetArgProCysSerLeuProProGlySerValLysSerLysTyr----- 109
Db 336 ATGAGACATCGATGCGGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 395
QY 109 ----- 109
Db 396 TCTCTCTCTCTCTCTCTCTCCGCGGTGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 455
QY 110 ---LysAspTyrTyrCysAlaLysGlyLysValSerLeuMetSerThrGlySerLeu 128
Db 456 GCAGCTTTCGGGAGCTGTTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 515
QY 129 HisGlnLeuHisIlePheIlePheValLeuAlaValPheHisValThrTyrSerValIle 148
Db 516 GAGCAGGTACACATTTCATCTTCCTGACGTATCCAGCAAGACGCTTCACGGCGCC 575
```


OY	149	lIeMelaLeuSerArgLeuLyMeTarqThTrpLySuLyStrpLuthGlnThAla	168
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Db	576	ACCGTCCCTCCGCGACCTTCCGACGTGGCGATATGGATCGACCTCGGAGAC-----	626
OY	169	SeLeuGlnLutGlnPheAlaMnArpGlnAlaArgPheArgThnHnGlnThSer	188
Db	621	ACCAATTGAGCAAGAGCGACCTCTCTCCCAAGATGATCGCCCGTGCAGAAATCAG	
		::: ::::	
OY	189	PheValLyS---ArgHnLyLeuSerSetThrProGly--lIeaTrpValVal	206
		::: :::: ::: :::	
Db	687	TTTCATCCAGACCGCGTGAAGGGTACAGAAAGCCCGCTGGGTATGATGATGGCTCGT	746
OY	207	AlaPheArgGlnPhePheArgSerValThrLyGlnValAspTrpLeuThLeuAlaAla	226
		::: ::: ::: ::: ::: ::: ::: :::	
Db	747	TCCTTCTCAAAAGTTCACAGATCAAGTCCCAAGACAGACATACATTCGATAGACTC	806
OY	227	GlyPheLeuAlaMnHnLyLeuSerHnHnSerLeuPheArPheHnLyStrpLLeuLy	246
		:::	
Db	807	GGTTTCCTCCAGACAGCTTGAAGGGCCACCCCAATTTCACTTTTACAGCATATGATC	866
OY	247	ArgSerMetGlnArpArPheLySuValValAlaGlylIeSerLeuProLeuTrpCysVal	266
		::: ::: ::: ::: ::: ::: ::: :::	
Db	867	AAACCTCTCAGAAAGATTTCAGACAGTGAATGAATGAATGAATGAATGAATGAATTTT	926
OY	287	AlaLeuLeuThrLeuPheLeuArpLLeaGlylIleGlyThrLeuThTrpLLeaSerPhe	286
		::: ::: ::: ::: ::: ::: :::	
Db	927	GTGATGATCTTTCTGCTGCTCAATGTCACCGGGTGGCACTCTTACTTGGATCTCATTA	986
OY	287	lIeProLeuVallIeLeuLyCysValGlylThrLyLeuGlnMetlIleMetGlnMet	306
		::: ::: ::: ::: ::: ::: ::: :::	
Db	987	GTTCACATGGCTCTGGTGGTTCATGGAGCAGCAACTGCACATCATAAACAGCTG	1046
OY	307	AlaLeuGlnlIleGlnArpArg-----AlaSerVallIleLyGlyAlaProValGln	324
		::: ::: ::: ::: ::: ::: :::	
Db	1047	GCGTACAGAGTGGCTCCGAGACAGCGCGGCAAGCGAAAGGGGAGCATGTGGTAC	1106
OY	325	ProSerAsnLyArPheThrPheHnLyArgProArpTrpValLeuPheHnLeu	344
		:::	
Db	1107	CCCTGGACAGCTGTGGTGGTCCGACGCCACCGGCTGTCTGTGTCATCCACTTC	1166
OY	345	ThrLeuPheGlnArpAlaPheGlnMetAlaHnLyPheValTrpThValAlAlaTrpGly	364
Db	1167	ATCTGTTCGAGAGCGGTGAGATTCGCTATTTCTTGTGGACATGGGAGATTTCCG	1226
OY	365	LeuLySuLyCysArPheHnMetHnLyLeuSerlIleMetLySuValValLeuGlyLeu	384
		:::	
Db	1227	GCGACATCTCGATCATGACAGACAGTCAAGATACAGCGTCTCGCAATCATATGCTC	1286
OY	385	AlaLeuGlnPheLeuLyCysSerTrpLlIeThrPheProLeuTrpAlaLeuValThrGlnMet	404
		:::	
Db	1287	GTCTCTCAGAGCTCTGCAAGTACAGCACTCCGCTCTTACCGCATCGTGTCCCATATG	1346
OY	405	GlySerAsnMetLySuArgSerlIePheArpGlnlIleThrAlaLyAlaLeuThrPheAsnTrp	424
		:::	
Db	1347	GGGAGTTCCTGTCAGAAAGCGCTGTGTGTGGAGACAGTCCGCGCAATTCAGAGGCTGG	1406
OY	425	ArgAsnThrAlaLyGlnLySuValArgAsnTrpLlIeArpMetLeuMetAlaGlnMet	444
		:::	
Db	1407	GCGGAGCGGCGCGAGCGCGTCCGG--AGATTCGCAAGGCTGTGACGCGCAATTCG	1466
OY	445	lIleGly---AspAlaThrProSerArgGlyThrSerProMetProSerArgAlaLeuSer	463
		:::	
Db	1464	CTGGGATACCGCGCGCGCGAGACGCGGCTGG-----GAAGCGCGCGCG	1508
OY	464	ProValHnLyLeuHnLyLyGlnMetGlyArgSerArpArpProGlnSerAlaProThr	483
		:::	
Db	1509	GCGTGAAGATTAAT-----GCGGAGAGCGGAGCGCGCCCAATCAAGCACTCGG	1558
OY	484	Ser-----ProArgThrMet	488
Db	1560	AGCATCTCTCTGAGTCTCTCTAGTTCTTGAGAAAGAAATCGAAAGCGCGCATCTGG	1619
OY	489	GlnGlnAla 491	

Db	1620	CAGCACGCG	1628
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		RESULT 5	
		US-09-183-959-11	
		; Sequence 11, Application US/09183959	
		; Patent No. 6303332	
		; GENERAL INFORMATION:	
		; APPLICANT: Cahoon, Rebecca E.	
		; APPLICANT: Miao, Guo-Hua	
		; APPLICANT: Rafalski, J. Antoni	
		; APPLICANT: Taramino, Graziana	
		; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE	
		; FILE REFERENCE: BB-1125	
		; CURRENT APPLICATION NUMBER: US/09/183,959	
		; CURRENT FILING DATE: 1998-11-02	
		; EARLIER APPLICATION NUMBER: 60/064,493	
		; EARLIER FILING DATE: No. 6303332member 5, 1997	
		; NUMBER OF SEQ ID NOS: 20	
		; SOFTWARE: Microsoft Windows 95	
		; SEQ ID NO. 11	
		; LENGTH: 1040	
		; TYPE: DNA	
		; ORGANISM: Zea mays	
		; US-09-183-959-11	
		Alignment Scores:	
		Pred. No.: 8,93e-78	Length: 1040
		Score: 745.50	Matches: 139
		Percent Similarity: 74.50%	Conservative: 48
		Best Local Similarity: 26.78%	Mismatches: 63
		Query Match: 4	Indels: 1
			Gaps: 1
US-09-857-896A-32 (1-534) x US-09-183-959-11 (1-1040)			
Oy	182	ATGPhetnhtHsglnthSerPheValLyArgHisLeuGly--LeuSerSerThrPro	200
Dd	1	AGGTTCACCCACGACGACTTCTGGTTTGAGGCACATATGATGTCACAAGAATTCCA	60
Oy	201	GLYLleatgrrvalVALalaphenhearglnrPhehatrgserVALlthryVALasp	220
Dd	61	GCATCCTTCTACATCAACAACTTCTCCGCGCATTTCTTAAGCTTCCGGTCGACAGCGGCACAC	120
Oy	221	TyrLeuthrLeuarGAlaIcylrPheLIeaSAlaHisLeuSerNHisaSerLySPheaSp	240
Dd	121	TACTCGCGGCTGCCACAGACTTTTGTCAAGCTCACTACCTGCGCCCTGGCACCAAGTTTGA	180
Oy	241	PHeNLsYtYrLIeUsArgrSerMetGLiasPAsPrPheLySVALlVALIGLYlleSer	260
Dd	181	TTSCAAAAGTACATCAACGCGCTCTGTGGAGAGACACTTCAAGGTATCTGGGGATCCAGC	240
Oy	261	LeuPrOLEutrcPYVALAlaleuuthrLeuPheLeuaspRIleaSPclYLleGlyThr	280
Dd	241	CCCTCTTGTGGGCTTCTCTCTCACTCTTCTCTTCTCAATGTCAATGGATGCGCACCC	300
Oy	281	LeuThrTrPLieserPheLIeProLeuVALilleLeuEucYSVALIGLYThrLySLeuGu	300
Dd	301	ATGCTCTGATCTCCATCAATGCGCGGTGTATCATCTGTCGCGGGGACGAAGCTGCAG	360
Oy	301	MeLIelleMetGIuestrALeUGluLIleGINasPrAGAlaSerVALilleysGLYAla	320
Dd	361	GGCATCATCTGCCGCTAGCGATGACATACAGAACGGGACAGCGCGGTATCCAGGGCATC	420
Oy	321	ProVALlGluproSerAnalysrPhehetrPheNHisarProAsprThrVALleuPhe	340
Dd	421	CGCGTGGGACAGGTGCACGACCTCACTTCTGGTTCCGACGCCCACTTCCTGCCTTTC	480
Oy	341	PhelIeNLSleuthrLeuPheDLiasAlaAPheGLImetAlaHisPheVALlthrVAl	360
Dd	481	CTCATCCACCTCACTCTTCTCAAGATGGTTTCCAGATCATCATCTCTCTCGATTTCTG	540
Oy	361	ALAthrProGLileuLysEucSerPheNHISmetNHISrIleGlyThrSerTLISmetThrA	380

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Db 541 TATGATGATGGGATGACCTGCTCTTCAACGACCTCCGAAGAATTCGCTTGTGACCTGTC 600
Qy 381 VALLLEUGLYLEUALALEUGLNPHELEUCYSSEYTYRLLIETHPHEPOLEUTYRALALEU 400
Db 601 TCCCTGGGGGTGGTGTTCAGAGCTGCTGACCTAGCGAGCGCTCCGTGATCGCGCTC 660
Qy 401 VALTRGIMETGLYSERASMETLYSARGSERLIEPHEASPGIUGINTHRLALYSALA 420
Db 661 GTCCTCCAGATGGGCTCCACCATGAGCAAGCATCTTCGACGAGACGACCTCCAGGCG 720
Qy 421 LEUTHASNTTPARGASNTHPRLALYSGLYLS 431
Db 721 CTCAGAACTGGCGCGCGGCCCAAGAAAG 753

RESULT 6
US-09-183-959-7
; Sequence 7, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 630332member 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 7
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-7

Alignment Scores:
Pred. No.: 3,08e-76 Length: 1831
Score: 736.00 Matches: 169
Percent Similarity: 53.80% Conservatve: 100
Best Local Similarity: 33.80% Mismatches: 174
Query Match: 26.44% Indels: 58
DB: 4 Gaps: 12

US-09-857-896a-32 (1-534) x US-09-183-959-7 (1-1831)
Qy 11 ArgThLeuProGluThrProSerTrpAlaValAlaLeuValPheAlaValMetIleIle 30
Db 91 CGGTGCGCTGGCGAGACGCCACCTGCTCCGTGGCAACCGTCACACCGCTCATGTCGCT 150
Qy 31 ValSerValLeuGluGlnAlaLeuGlnAlaLeuGlnAlaLeuGlnAlaLeuGlnAlaLeu 50
Db 151 GCCTGCTCTCTGTCGACGCTCCCTCTGCGCTTGGCCAACTGGCTGCGCAAGACCAAG 210
Qy 51 LysAsnAlaLeuAlaGluAlaLeuGlnLysIleLysAlaGluLeuMetLeuValGlyPhe 70
Db 211 CGGAAGCCCATGCTCGCGCGCTCGAAGAAAGATCCGGAAGACTGATGCTGCTCGAGTGC 270
Qy 71 IleSerLeuLeuAlaValAlaThrGlnAspProIleSerGlyIleCysIle---SerGlu 89
Db 271 ATCTGCTGCTCTGTCAGCAAGACGCGCGCTTCATATCGGAAGATGCGATGCGCTCGT 330
Qy 90 LysAlaIleSerIleMetArgProCysSerLeuProGlySerValLysSerLysTyr 109
Db 331 CTCCTACACGCGCTTCTACATCTGCTCC-----GAGAGGAGACTAG 372
Qy 110 LysAsp----- 111
Db 373 CAGGACCTGCTCTGCGCAACAGGACGCCAACCAGAGCGGCTTGACAGAACATGTTGGT 432
Qy 112 -----TyrTyrCysAlaLysLysGlyLysValSerLeuMetSerThrGlySer 127
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Db 433 GGGCAAGCGCTGACCTGTGGCC---GAGGGCAATGAACTTTGTTCTTCCAGAGGCG 489
Qy 128 LeuHisGlnLeuHisIlePheIlePheValLeuAlaValPheHisValThrTyrSerVal 147
Db 490 CTTAGAGAGCTGACCGGTTTCTCTCATCTTGGATGATCAATCATCTGTGTACAGTTT 549
Qy 148 IleIleMetAlaLeuSerArgLeuLysMetArgThrTyrLysLysTrpGluThrGluThr 167
Db 550 GTACAGTGTGCTGCTCATGATCAAGATCATAGCTGAGGAGGAGGAGGAGGAGGAGGAGG 603
Qy 168 AlaSerLeuLysGlnPheAlaAsnAspProAlaArgPheThrPheThr----- 184
Db 604 -----TTACAGCTCAATTGCTCTGAGGAATGGAACCTAGGAGAACCAAGAGTATG 657
Qy 185 ---HisGlnThrSerPheValLysArgHisLeuGly-----LeuSerSerThrProGly 201
Db 658 AGAAGCAGCATCTTGTGTTTAAACATCTTCATATCCATGAGCAAAAATTAATA 717
Qy 202 IleArgTrpValAlaAlaPhePheArgGlnPhePheArgSerValThrLysValAspTyr 221
Db 718 CTATTTGGATGCTTGTGCTTTTGGGTCATATTCAGAGGCTCCATATATAGTCAGACTAT 777
Qy 222 LeuThrLeuArgAlaGlyPheIleAsnAlaHis---LeuSerHisSerLysPheAsp 240
Db 778 TTGGCACTGAGGTGGGCTTGTGTCATATCACAAGCTACACCATCA-----TATGAC 831
Qy 241 PheHisLysTyrLysLysArgSerMetGluAspAspPheLysValValValGlyLysSer 260
Db 832 TTCCATTAATACATGTGTACGAGGAGCATGAGATATATACATGAGCAATATGTGATCAGT 891
Qy 261 LeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspLysGlyLysGlyThr 280
Db 892 TGGCACTTGGGCAATATGCTTCGATATTAATCAATGATCATGATGATCAATATA 951
Qy 281 LeuThrTrpLysSerPheIleProLeuValIleLeuLeuGlyValGlyThrLysLeuGlu 300
Db 952 TATTTCTGCTGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
Qy 301 MetIleIleMetGluMetAlaLeuGluIleGlnAspArgLysAspValIleLysGlyValA 320
Db 1012 CACGTCAATGCTCAGATGCTGTTGGAACTGCTGAGCAACAGCGCTTAATGTTGGCTCA 1071
Qy 321 ProValAlaGluProSerAsnLysPhePheThrPheHisIleArgProAspTrpValLeuPhe 340
Db 1072 CAA---CTTAACGCGGTGATGATCTATTTGTTGGAAGCGCTGCGTACTCGGTGG 1128
Qy 341 PheIleHisIleuThrIleuPheGlnAsnAlaPheIleMetAlaHisPheValThrPheVal 360
Db 1129 CTATACAGATTCATTTCAATTCAGAAATGCTTTTGAAGCTGCAACATCTTATAGTCTCTG 1188
Qy 361 AlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysVal 380
Db 1189 TGGGAACCTAGTGCAACAAACATGTTTCATGAAGCACTACATACATGCTGCTGCTGCTG 1248
Qy 381 ValLeuGlyLeuAlaLeuGlnPheLeuGlySerTyrLlePhePheProLeuLysAlaLeu 400
Db 1249 ATTCTGGGCTCTTAGTCAATTTGTTGGAGCTACAGCAACACTCCCGCTGAATGTATTT 1308
Qy 401 ValTrgImetGlySerAsnMetLysArgSerIlePheAspGluInThrAlaLysAla 420
Db 1309 ATTTCTGAGATGGGTCCCAAGTTCAAGAAATCACTGCTGCGAAGACGTGAGGAGTGC 1368
Qy 421 LeuThrAsnTrpArgAsnThrAlaLysGluLysLysValArgAspThrAspMetLeu 440
Db 1369 CTGCAAGAGCTGG-----TGCAAGAGGGTGAAGACAG-GAGCGCAGA 1409
Qy 441 MetAlaGlnMetIleGlyAspAlaThrProSerArgLysThrSerProMetPro----- 458
Db 1410 CAATCCGCTCTTCTCGGAGAGGAGCCTCAGCAACAGATCGGTGCTGCTCCCTGACAC 1469
Qy 459 -----SerArgAlaSerSerProValHisIleuMetHisLysLysMetGly 473
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Db 1470 CACCTACGACGCGATCAGACAGACGCGTGTGCACCGCTGTGCAGACGCGTGC 1529

RESULT 7

US-09-183-959-13

; Sequence 13, Application US/09183959

; Patent No. 6303332

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Rafalaki, J. Antoni

; APPLICANT: Taramino, Graziana

; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE

; FILE REFERENCE: BB-1125

; CURRENT APPLICATION NUMBER: US/09/183,959

; EARLIER FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: 60/064,493

; EARLIER FILING DATE: No. 6303332ember 5, 1997

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Microsoft Windows 95

; SEQ ID NO 13

; LENGTH: 538

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (479)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (492)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (499)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (518)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (530)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (537)

; US-09-183-959-13

Alignment Scores:

Pred. No.:	7	28e-59	Length:	538
Score:	580.50	Matches:	114	
Percent Similarity:	74.86%	Conservative:	23	
Best Local Similarity:	62.30%	Mismatches:	38	
Query Match:	20.85%	Indels:	9	
DB:	4	Gaps:	3	

US-09-857-896a-32 (1-534) x US-09-183-959-13 (1-538)

Qy 323 ValGluProSerAsnLysPhePheTrpPheHisArgProAspTrpValLeuPhePheIle 342

Db 1 GTGGAGCCAAAGTACAGAGTCTTCTGTGTTAACCGCCGCTGGGTGCTCTTCCTCATC 60

Qy 343 HisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheValTrpThrValAlaThr 362

Db 61 CACCTACGCGCTCTCCAGACGCGCTCCAGATGGCCATTGCTTGGACACCTCTAC 120

Qy 363 ProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetLysValValLeu 382

Db 121 CCGACCTGAAAGAAATGCTACCAAGAGCGCTGGCTGAGCATATGAAGTTGCGGTG 180

Qy 383 GlyLeuAlaLeuGlnPheLeuCysSerTrpIleThrPheProLeuTrpAlaLeuValThr 402

Db 181 GGGCTGGTCTCCAGAGTCTCTGCAGCTACATCAGCTCCCGCTAGCGCGCTGACG 240

Qy 403 GlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThrAlaLysAlaLeuThr 422

Db 241 CAGATGGGCTCCACATGAAAGAACCATCTCTGAGGAGACAGCGCCAGCGCGTGATG 300

Qy 423 AsnTrpArgAsnThrAlaLysGlyLysLysValArgAspThr-----Asp 438

Db 301 AAGTGGCGAAGACCGCCCAAGGATTAAGTGGCCGCGCGAGCGCGCTTCCTGCAC 360

Qy 439 MetLeuMetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSerPrometPro 458

Db 361 GTGCTGACGAGC-----GCCGACACCGACCGCGACACAGCCCGGAGCTGCGCG 411

Qy 459 SerArgAlaSerSerProValHisLeuLeuHisLysGlyMetGlyArgSerAspAspPro 478

Db 412 AGCGGGGCAACTGCGCGGTGCACCTGCTCCACAAAGTACAGGCGCGAGTGGAGAACCG 471

Qy 479 GlnSerAlaProThrSerProArgTrpMetGluGlnAlaArgAspMetTrpProValVal 498

Db 472 CAGAGGAGNCCGCGCGTGC-----CGNCGCGCGNAGCTTGGG-GAAATGTANCGGTGCT 527

Qy 499 ValAlaHis 501

Db 528 GANCAACAT 536

RESULT 8

US-09-183-959-17

; Sequence 17, Application US/09183959

; Patent No. 6303332

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Rafalaki, J. Antoni

; APPLICANT: Taramino, Graziana

; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE

; FILE REFERENCE: BB-1125

; CURRENT APPLICATION NUMBER: US/09/183,959

; EARLIER FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: 60/064,493

; EARLIER FILING DATE: No. 6303332ember 5, 1997

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Microsoft Windows 95

; SEQ ID NO 17

; LENGTH: 705

; TYPE: DNA

; ORGANISM: Zea mays

; US-09-183-959-17

Alignment Scores:

Pred. No.:	5	.02e-40	Length:	705
Score:	422.00	Matches:	91	
Percent Similarity:	53.02%	Conservative:	32	
Best Local Similarity:	39.22%	Mismatches:	36	
Query Match:	15.16%	Indels:	74	
DB:	4	Gaps:	3	

US-09-857-896a-32 (1-534) x US-09-183-959-17 (1-705)

Qy 182 ArgPheThrHisGlnThrSerPheValLysArgHisLeuGly----LeuSerSerThrPro 200

Db 2 AAGTTCACCCAGAGAGACTTCTCGTAGGAGCAGATATGATGTGTAACAAAGTTCCCA 61

Qy 201 GlyIleArgTrpValValAla----- 207

Db 62 GCATCATCTTCAATCGTAAATAGATTGAATTCAATTCATTCGATCTAATATATATGC 121

Qy 208 -----PhePhe 209

Db 122 TAGTAGCTACGACGAGTGCATAGACTGACGACGACATATATGACAGAACATCTTTC 181

Qy 210 ArgGlnPhePheArgSerValThrLysValAspTrpLeuThrLeuArgAlaGlyPheIle 229

Db 182 CGGAGTCTTCAAGTCCGAGGAGCGAGGAGACTATGCGCGCTGCGCCACAGCTTTGTC 241

Qy 230 AsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLysTrpIleLysArgSerMet 249

Db 242 AACGTCTATCTGGCCCTCGACGACAAAGTTTGAATTTCAGAAATACATCAAGCGGTCTCTG 301

```

Qy 250 GIUASpApPhelYsValValIglYIlleSerLeuProLeuTrpCysValAlaIleLeu 269
    |||||
Db 302 GAGGATGACTTCAGAGCTGATCGTGGGATCACTCTCTGTGGCTTGTGCTCATC 361
Qy 270 ThrLeuPheLeuAspIleAspIleGly----- 279
    |||||
Db 362 TTCCTTCCTCAACGTCATGGTACGTA-CGTATACGTAGGGTGTTCGAGATCGAGA 420
Qy 279 ----- 279
Db 421 TCCATGCATGCATCTCTCATCTATATATATATATATATATATATATATATATAT 480
Qy 280 -----ThrLeuThrTrpIleSerPheIlePro 288
    |||||
Db 481 CTGGCTGCATGATCATGATGATGAGATGGACACCATCTCTGGATCTCCATCATCGCG 540
Qy 289 LeuValIleLeuLeuCysValIglYThrIleuGluMetIleIleMetGluMetAlaLeu 308
    |||||
Db 541 GTGGTGCATCATCTGTGGTGGGAGAGAGTGCAGGGCATCATCTGCCCATGGCGATC 600
Qy 309 GluIleGlnAspArgAlaSerValIleYsGlyAlaProValValIgluProSerAsnLys 328
    |||||
Db 601 GACATTCAGGAGGCGCACGCCGTATCCAGGGCATCCGATGTGCAAGTCAGCGACTCC 660
Qy 329 PhePheTrpPheHisArgProAspTrpValLeuPhe 340
    |||||
Db 661 TACTTCTGTGGTGGCGCCGACCTTCGTGCTCTTT 696

RESULT 9
US-09-183-959-18
; Sequence 18, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tarantino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO: 18
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-18

Alignment Scores:
Pred. No.: 9,56e-37 Length: 750
Score: 394.50 Matches: 91
Percent Similarity: 50.61% Conservative: 34
Best Local Similarity: 36.84% Mismatches: 34
Query Match: 14.17% Indels: 89
DB: 4 Gaps: 5

US-09-857-896a-32 (1-534) x US-09-183-959-18 (1-750)
Qy 182 ArgPheThrHisGlnThrSerPheValIleYsArgHisLeuGly----LeuSerSerThrPro 200
    |||||
Db 2 AGGTTACCCACGAGACTTCCTTTGTGAGGACATATGATGTGCTCAACAAAGTTCCCA 61
Qy 201 GlyIleArgTrpValAlaIle----- 207
    |||||
Db 62 GCATCTCTTACATCGTAAATCATGATGCTTTCTACTGAATTTGTGTATTCATTT 121
Qy 208 -----PhePheArgGlnPhePheArgSer 215
    |||||
Db 122 GCATCTGAGCATCATGATGCTGCTGCGAGACACTTCTTCGCGACTTCTTCAGGTCC 181

```

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Qy 216 ValThrIleYsValAspTrpIleThrLeuArgAlaGlyPheIleAsnAla----- 231
    |||
Db 182 GTCAGGGGAGGACAGACTACTGCGCGCTGGCGACAGAGCTTTGTCAAGT-ATGTAGGGCCAC 240
Qy 231 ----- 231
Db 241 GCCAGCTTTGTTGCTGCTCTTTCATTTGGCATACAGACCAACAATGATATATAT 300
Qy 232 -----HisLeuSerHisAsnSerLysPheAspPheHisLysTrpIleYsArg 247
    |||||
Db 301 CGTATGAGGTCCATCTGGCCCGTGGACCAAGTTGATTTCCAAAGATCATCAAGCGG 360
Qy 248 SerMetGlnAspAspPheYsValValIglYIleSerLeuProLeuTrpCysValAla 267
    |||||
Db 361 TCTGTGAGGACCATCTTCAAGGTGATGCTGGGGATCAGCCCTCTTGTGGGCTTCTGCT 420
Qy 268 IleLeuThrPheLeuAspIleAspIleY----- 277
    |||||
Db 421 CTCACTTCTTATCTCTCAATGTCAATGTATATATATATATATATATATATATATAT 480
Qy 278 -----IleGly----- 279
    |||||
Db 481 TTACCTTAGCTAGGTAATATAGGTCGTCCATCATGCATCTGACGACGATGCATATAT 540
Qy 280 -----ThrLeuThrTrpIleSerPheIleProLeuValIleLeu 293
    |||||
Db 541 ATATATGACAGATGGCACACCATCTCTGTGATCTCCATCATGCGGGTGTGATCATCTG 600
Qy 294 CysValIglYThrIleuGluMetIleIleMetGluMetAlaLeuGlnIleGlnAspArg 313
    |||||
Db 601 TCGTGTGGAGCAAGCTGCAGAGGCACTCATCTGCCGATGCGCATGCAGATCAGGAGCGG 660
Qy 314 AlaSerValIleYsGlyAlaProValValIgluProSerAsnLysPhePheHis 333
    |||||
Db 661 CACCCCGTATCCAGGCGCATCCCGCTGTGAGGTGACGACGACTCTGCTGTTGCA 720
Qy 334 ArgProAspTrpValLeuPhe 340
    |||||
Db 721 CGCCCAACCTTCGTGCTCTTT 741

RESULT 10
US-09-183-959-3
; Sequence 3, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tarantino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO: 3
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (475)
; NAME/KEY: unsure
; LOCATION: (520)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (538)

```

```

FEATURE:
? NAME/KEY: unsure
? LOCATION: (540)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (552)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (559)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (568)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (571)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (583)
US-09-183-959-3

```

```

Alignment Scores:
Pred. No.: 8.37e-26 Length: 597
Score: 300.00 Matches: 71
Percent Similarity: 59.41% Conservative: 30
Best Local Similarity: 41.76% Mismatches: 67
Query Match: 10.78% Indels: 5
DB: 4 Gaps: 1

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US-09-857-896a-32 (1-534) x US-09-183-959-3 (1-597)

```

OY 232 H1sleuSerHisAsnSerLysPheAspPheHisLysTyrIleLysArgSerMetGluAsp 251
Db 12 CACATCCGAGAAACAGATATGATTTCCACAAATACATGACGCGGTGGAATAT 71
OY 252 AspPheLysValValValValIleLysLeuProLeuTyrCysValAlaIleLeuThleu 271
Db 72 GAGTTTAAAGACTGTGTGATCAGCTGATCTGTGGCTTTTGTAATCTTATTCCTG 131
OY 272 PheLeuAspIleAspIleLysGlyIleGlyThleuThrTrpIleSerPheIleProLeuValIle 291
Db 132 CTGCTGAATATAATGATGATGACACATCTCTGCTGCTTCTGCTCTATTTCTG 191
OY 292 LeuLeuCysValGlyThrLysLeuGluMetIleIleMetGluMetAlaLeuGluIleGln 311
Db 192 TTACTTATGTTGGTGGCCAACTAGACACATATATCAGCTGCTGCTTCAGAGGACGCG 251
OY 312 ---AspArgAlaSerValIleLysGlyAlaProValValGluProSerAsnLysPhe 330
Db 252 ATATCATTTATCAAAATATATACAGAGAGATTCCGAAATATAAGCCATGACAGACCATTTTC 311
OY 331 TrpPheHisArgProAspTrpValLeuPhePheIleHisLeuThleuPheGlnAsnAla 350
Db 312 TGGTTTCACAGCGCTAGCTAGCTCTTATGATTCATTCATTCATTCCTTTCACAAATTCG 371
OY 351 PheGluMetAlaHisPheVal-TrpThrValAlaThrProGlyLeuLysCysPheH1 370
Db 372 TTGAGATTAAGTTTCTCTCTGATTCGATTCAGAGAGTTTCGGTTCGTATGATAT 431
OY 370 smetHisIleGlyLeuSerIleMetLysValValLeuGlyLeuAlaLeuGlnPheLysCys 390
Db 432 GGAACGGAA-GCTTATGTCATTTCCAGCTTGTATTCGGGTG-ATNATTCGAAGTCACCTG 489
OY 390 sSerTrpIleThrPheProLeuTyrAla 399
Db 490 CAGCTATATCCCG-CCACTATACGCA 516

```

```

RESULT 11
US-09-183-959-5
; Sequence 5, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua

```

```

? APPLICANT: Rafalski, J. Antoni
? APPLICANT: Taramino, Graziana
? TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
? FILE REFERENCE: BB-1125
? CURRENT APPLICATION NUMBER: US/09/183,959
? EARLIER FILING DATE: 1998-11-02
? EARLIER APPLICATION NUMBER: 60/064,493
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: Microsoft Windows 95
? SEQ ID NO 5
? LENGTH: 472
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (164)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (351)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (379)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (398)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (414)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (427)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (439)..(440)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (447)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (450)
US-09-183-959-5

```

```

Alignment Scores:
Pred. No.: 5.47e-07 Length: 472
Score: 138.50 Matches: 37
Percent Similarity: 52.69% Conservative: 12
Best Local Similarity: 39.78% Mismatches: 31
Query Match: 4.97% Indels: 14
DB: 4 Gaps: 3

```

US-09-857-896a-32 (1-534) x US-09-183-959-5 (1-472)

```

OY 375 LeuSerIleMetLysValValLeuGlyLeuAlaLeuGlnPheLysCysSerTrpIleThr 394
Db 138 CTTCCTACTTCAGAGGCGGTATTCANCTT-----CTTCACACTCAGACACC 185
OY 395 PheProLeuTyrAlaLeuValThrGlnMetGlySerAsnMetLysArgSerIlePheAsp 414
Db 186 TTGCCTCTGTATGCAATTTATACCCAGATGGGAGACTCTTCACAGAGGATCTTCACAC 245
OY 415 GluGlnThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLysVal 434
Db 246 GAGCATGTGCGAGCGGCGCTCGGCGCTGCGTCAGAGGTCAAGTCAAGAAAGGAGACTG 305
OY 435 ArgAspTrpAspMetLeuMetAlaGlnMetIleGlyAspAlaThrProSerTrpGlyThr 454
Db 306 AGGAGAGCTGCATCTGCTA-----GCAAGGACGATCTGTA----- 340
OY 455 SerProMetProSerAlaGalaSerTrpProValHisLeu 467
Db 341 ---CCAATGCCGANTCGGAGGAGCACTTCGTTAAGATTG 376

```


Alignment Scores:

Pred. No.: 4.04 Length: 6315
 Score: 96.50 Matches: 44
 Percent Similarity: 39.39% Conservative: 34
 Best Local Similarity: 22.22% Mismatches: 89
 Query Match: 3.47% Indels: 31
 DB: 3 Gaps: 7

US-09-857-896A-32 (1-534) x US-08-772-512A-2 (1-6315)

```

QY 346 Leupheglnasnlaphheglnmetalahtshphevaltrphrvalalathrproglyleu 365
    |||:|||||:|||||
DB 1144 CTGTATACAGCAGCTGCTGCAGACAGCTGGA---CCCTGG-----1179
QY 366 Lyslyscyspshhehismethisileglyleuserillemetlysalvalleuglyleuala 385
    |||:|||||:|||||
DB 1180 -----CACATGTTGTTCTTATAGTCATCATCTTCTAGT-----1215
QY 386 Leuglnpheleucyserrytlierhrpheproleutyralaleuvalthrnglmetgly 405
    |||:|||||:|||||
DB 1216 -----TCATTCTATCTTGATTTGATTTGGCCATTTGTCCTTAT 1263
QY 406 Serasmetlysarqserilrheaspluglnthrila-----Lysalaleuthrasn 423
    |||:|||||:|||||
DB 1264 GACGAATTGCCAAGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323
QY 424 Trpargasnthralalysglulys---Lyslysalalargasprhrasphmetleumetala 442
    |||:|||||:|||||
DB 1324 GCTGAAGAGCGGCGAGCAGCCAGAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
QY 443 Glmetlileglyasphalathrproserarglythrserprometproserarglaser 462
    |||:|||||:|||||
DB 1384 CAACGGGCTCAGATGACAGCGGATGCCCTCGGACAGCTTCATCCAGATGGCAAG 1443
QY 463 Serprovalhis-----Leuethislysglymetglyraserp 476
    |||:|||||:|||||
DB 1444 AGTCCACAGTACTCTTGATAGTATGACTGTTTGTGGCGGCGAGAGAGAGAGAGAGAGAT 1503
QY 477 Aspproglinseralarprothserproargthmetgluglnlaargasphmetlyrpro 496
    |||:|||||:|||||
DB 1504 GACAAACAAGAGAGAGAGATGCGATACGACGCTCGAGATGAGATGAGAGAGAGAGAGAG 1563
QY 497 Valvalvalalalansprovalhisargyleuansproalaspargthrasmetlyser 516
    |||:|||||:|||||
DB 1564 GTTATACAAAGACAGACACCTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623
QY 517 Sereralaleuaspalaspilrproseralaspsheserphesererglly 534
    |||:|||||:|||||
DB 1624 ACGACTTCCTTA-----TCCTTACCTGGTTCCACATTTTAACTAGCGCGGGA 1671

```

RESULT 14

US-08-808-793-1
 ; Sequence 1, Application US/08808793
 ; Patent No. 5858713

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.
 APPLICANT: Ingles, Patricia J.
 TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 STREET: Clinton Square, P.O. Box 1051
 CITY: Rochester
 STATE: New York
 COUNTRY: USA
 ZIP: 14603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808,793
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,361
 FILING DATE: 24-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/012,649
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Braman, Susan J.
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 716-263-1636
 TELEFAX: 716-263-1600
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6318 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

US-08-808-793-1

Alignment Scores:

Pred. No.: 4.04 Length: 6318
 Score: 96.50 Matches: 44
 Percent Similarity: 39.39% Conservative: 34
 Best Local Similarity: 22.22% Mismatches: 89
 Query Match: 3.47% Indels: 31
 DB: 2 Gaps: 7

US-09-857-896A-32 (1-534) x US-08-808-793-1 (1-6318)

```

QY 346 Leupheglnasnlaphheglnmetalahtshphevaltrphrvalalathrproglyleu 365
    |||:|||||:|||||
DB 1144 CTGTATACAGCAGCTGCTGCAGACAGCTGGA---CCCTGG-----1179
QY 366 Lyslyscyspshhehismethisileglyleuserillemetlysalvalleuglyleuala 385
    |||:|||||:|||||
DB 1180 -----CACATGTTGTTCTTATAGTCATCATCTTCTAGT-----1215
QY 386 Leuglnpheleucyserrytlierhrpheproleutyralaleuvalthrnglmetgly 405
    |||:|||||:|||||
DB 1216 -----TCATTCTATCTTGATTTGATTTGGCCATTTGCCATGCTTAT 1263
QY 406 Serasmetlysarqserilrheaspluglnthrila-----Lysalaleuthrasn 423
    |||:|||||:|||||
DB 1264 GACGAATTGCCAAGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323
QY 443 Glmetlileglyasphalathrproserarglythrserprometproserarglaser 462
    |||:|||||:|||||
DB 1384 CAACGGGCTCAGATGACAGCGGATGCCCTCGGACAGCTTCATCCAGATGGCAAG 1443
QY 463 Serprovalhis-----Leuethislysglymetglyraserp 476
    |||:|||||:|||||
DB 1444 AGTCCACAGTACTCTTGATAGTATGACTGTTTGTGGCGGCGAGAGAGAGAGAGAGAT 1503
QY 477 Aspproglinseralarprothserproargthmetgluglnlaargasphmetlyrpro 496
    |||:|||||:|||||
DB 1504 GACAAACAAGAGAGAGATGCGATACGACGCTCGAGATGAGATGAGAGAGAGAGAGAG 1563
QY 497 Valvalvalalalansprovalhisargyleuansproalaspargthrasmetlyser 516
    |||:|||||:|||||
DB 1564 GTTATACAAAGACAGACACCTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623

```

QY 517 SerSerAlaLeuAspAlaSerPheProSerAlaAspPheSerGlnGly 534
DB 1624 ACACACTTCCTTA-----TCCTTACCTGGTTCACCATTTAACTTACCGCGGGGA 1671

RESULT 15
US-08-772-512A-1

; Sequence 1, Application US/08772512A
; Patent No. 6022705
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Knipple, Douglas C.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
; TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,512A
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,618
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/601(CRPD-1657)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1600
; TELEFAX: 716-263-1636
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-772-512A-1

Alignment Scores:

Pred. No.: 4.04 Length: 6318
Score: 96.50 Matches: 44
Percent Similarity: 39.39% Conservative: 34
Best Local Similarity: 22.22% Mismatches: 89
Query Match: 3.47% Indels: 31
DB: 3 Gaps: 7

US-09-857-896A-32 (1-534) x US-08-772-512A-1 (1-6318)

QY 346 LeuPheGlnAsnAlaPheGlnMetAlaHisPheValITrPnValAlaIAlaItnProGlyLeu 365
DB 1144 CTGTATACACGACGTCTGCACAGCAGTGA--CCCTGG----- 1179
QY 366 LysLysCysPheHisMetHisIleGlyLeuSerIleMetLysValValLeuGlyLeuAla 385
DB 1180 -----CACATGTGTCTTTATATAGTATCATCATCTTCCCTAGT----- 1215
QY 386 LeuGlnPheLeuCysSerTyrIleTrpPheProLeuTyrAlaLeuValItnGlnMetGly 405
DB 1216 -----TCATTTCTATCTTGATTTGAAATTGATTTTGGCCATTTGGCCATTTGCCATGCTCTAT 1263

QY 406 SerAsnMetLysArgSerIlePheAspGluGlnThrAla-----LysAlaLeuThrAsn 423
DB 1264 GACGATTTGCAAAAGAGAGCCGAAAGAAAGAGGCTGCCGAGAGAGAGCGCATACGAGAA 1323
QY 424 TrpArgAsnThrAlaLysGlyLys---LysLysValArgAspThrAspMetLeuMetAla 442
DB 1324 GCTGAGAAAGCGGACAGCCAGCCAGCGCCAAACTGTGAGAGAGCGGGCCAAATGTAGCAGT 1383
QY 443 GlnMetIleGlyAspAlaThrProSerArgGlyThrSerProMetProSerArgAlaSer 462
DB 1384 CAAAGCGCTCAGATGCGACGCGGATGCCGCTGCCGACGCTCTGCATCCGGAATGCGAAAG 1443
QY 463 SerProValHis-----LeuLeuHisLysGlyMetCylArgSerAsp 476
DB 1444 AGTCCACGTACTGTGATTAAGCTTAAGTAAGTCTGTTGGCGGAGAGAGCGGACGAT 1503
QY 477 AspProGlnSerAlaProThrSerProArgThrMetGluGluAlaArgAspMetLysPro 496
DB 1504 GACACACAAAGAGAGAGATGTCATTAAGCGAGGTGGAATCGGATCGGTGAGC 1563
QY 497 ValValValAlaHisProValHisArgLeuAsnProAlaAspArgArgValSer 516
DB 1564 GTTATACAAAGACCAACACACACACACACCGCTACTTAAGTCCGTAAGTTAGC 1623
QY 517 SerSerAlaLeuAspAlaSerPheProSerAlaAspPheSerGlnGly 534
DB 1624 ACACACTTCCTTA-----TCCTTACCTGGTTCACCATTTAACTTACCGCGGGGA 1671

Search completed: November 18, 2002, 17:14:00
Job time : 77 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame-plus_p2n model

Run on: November 18, 2002, 16:40:53 ; Search time 60 Seconds
(without alignments)
3288.658 Million cell updates/sec

Title: US-09-857-896a-32

Perfect score: 2784
Sequence: 1 MAEDYEPPARTLPETPSMA.....VSSALADIPSADEFPSOG 534

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328367 segs, 184756068 residues

Total number of hits satisfying chosen parameters: 656734

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: Published.Applications.NA:*

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- 5: /cgn2_6/ptodata/1/pubpna/PC7S_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1241	44.6	1752	9	US-09-938-842A-1680
3	1160.5	41.7	1710	9	US-09-938-842A-1347
4	1106	39.7	1725	9	US-09-938-842A-1689

5	955	34.3	1491	9	US-09-938-842A-2268	Sequence 2268, Ap
6	932.5	33.5	1581	9	US-09-938-842A-1086	Sequence 1086, Ap
7	465	16.7	1007	10	US-09-770-445-226	Sequence 226, App
8	447.5	16.1	471	10	US-09-770-444-164	Sequence 164, App
9	346.5	12.4	448	10	US-09-770-444-733	Sequence 733, App
10	338	12.1	396	10	US-09-878-574-1249	Sequence 1249, Ap
11	220.5	7.9	279	10	US-09-878-574-13167	Sequence 13167, A
12	159	5.7	455	10	US-09-924-035A-887	Sequence 887, App
13	159	5.7	457	10	US-09-770-444-512	Sequence 512, App
14	142	5.1	268	10	US-09-923-876-2134	Sequence 2134, Ap
15	108	3.9	2010	12	US-10-033-717-9	Sequence 9, App11
16	98	3.5	1153	10	US-09-974-300-2667	Sequence 2667, Ap
17	98	3.5	1713	10	US-09-887-576-809	Sequence 809, App
18	97	3.5	155074	9	US-10-026-188-6	Sequence 6, App11
19	94.5	3.4	1755	10	US-09-954-456-1166	Sequence 1166, Ap
20	92	3.3	1195	10	US-09-759-143-878	Sequence 878, App
21	92	3.3	1195	10	US-09-780-669-878	Sequence 878, App
22	92	3.3	1195	10	US-09-822-827-878	Sequence 878, App
23	92	3.3	3915	10	US-09-822-827-878	Sequence 878, App
24	92	3.3	21721	10	US-09-764-853-861	Sequence 861, App
25	92	3.3	27360	10	US-09-070-927A-164	Sequence 164, App
26	91	3.3	1835	10	US-09-216-393-80	Sequence 80, App1
27	91	3.3	6083	9	US-10-029-413A-21	Sequence 21, App1
28	90.5	3.3	2332	9	US-10-045-815-7	Sequence 7, App11
29	90.5	3.3	2416	9	US-10-045-815-5	Sequence 5, App11
30	90.5	3.3	24023	9	US-10-094-679-1	Sequence 1, App11
31	90	3.2	2829	9	US-10-045-815-1	Sequence 1, App11
32	89.5	3.2	74586	10	US-09-781-558-3	Sequence 3, App11
33	89	3.2	2024	10	US-09-867-569-1	Sequence 1, App11
34	89	3.2	5520	9	US-09-902-525-38	Sequence 38, App11
35	88.5	3.2	1068	10	US-09-864-761-26799	Sequence 26799, A
36	88.5	3.2	1422	10	US-09-864-761-10158	Sequence 10158, A
37	88.5	3.2	3168	10	US-09-880-107-2099	Sequence 2099, Ap
38	88	3.2	1443	10	US-09-974-300-2883	Sequence 2883, Ap
39	88	3.2	1797	10	US-09-878-764-3	Sequence 3, App11
40	88	3.2	2733	10	US-09-878-764-1	Sequence 1, App11
41	87.5	3.1	1132	10	US-09-729-674-23	Sequence 23, App1
42	87	3.1	1083	10	US-09-974-300-2681	Sequence 2681, App
43	87	3.1	1256	10	US-09-822-830A-217	Sequence 217, App
44	87	3.1	1803	10	US-09-887-576-812	Sequence 812, App
45	87	3.1	1900	10	US-09-828-313-19	Sequence 19, App1

ALIGNMENTS

RESULT 1
US-09-938-842A-2048
Sequence 2048, Application US/0938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepes, Joel
APPLICANT: Zhu, Tong
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2048
LENGTH: 1713
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2048
Alignment Scores:

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NUMBER OF SEQ ID NOS: 5379

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; SEQ ID NO 1680
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; LENGTH: 1752
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; TYPE: DNA
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1680
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Score:	1241.00
Percent Similarity:	64.16%
Best Local Similarity:	47.59%
Query Match:	4 4.58%
DB:	9
Gaps:	6
Length:	175
Matches:	247
Conservative:	86
Mismatches:	18
Indels:	48
Gaps:	6

US-09-857-896A-32 (1-534) x US-09-938-842A-1680 (1-1752)

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Qy	31	ValSerValLeuLeuGluIuhIsAlaLeuHisIuLeuGluYhNstRPhenIsIuSArgHis	50
Db	82	AAATGGATCGTGTATATGAGAAACCTTATTCATTAATAATTTGATCTCGTGTAAAAAGAAAC	141
Qy	51	LysAsnAlaLeuAlaGluValAlaLeuGluYhIuLeuValGluIuLeuMetLeuValGlyPhe	70
Db	142	AAAAAGGCTCATATGAGACACTGAAAAAGTAAAGTAAAGCAGACCTTATGCGATGGATTC	201
Qy	71	IleSerIleuLeuAlaValAlaThrGlnAspProIleSerGlyIleCysIleSerGluIuys	90
Db	202	AAATACACTACTTCAACCAATTTGGACAAAGATATATCTCAAAATATTCATCTTAAGAAC	261
Qy	91	AlaAlaSerIleMetArgProSer-----	99
Db	262	ATCGGACGATGATGACCCCTTGATGTCATCCGAAAGAACAAAGATGTGTAAAGAA	321
Qy	99	-----	99
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Qy	100	-----LeuProProGluSerValIuYserIuSerIuValuAspTyrTyrCysAlaIuSlys	117
Db	382	TCGCTTATCTCGTGAAGAGATTGGCTACATAAGTTATGAT-----AGTGTGAGAGAA	438
Qy	118	GlyIuValSerIeuleuMetSerThrIleYserIuHisGlnLeuHisIlePheIlePheVal	137
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Qy	138	LeuAlaValPheHisIuAlaThrIuYserValIleIleMetAlaLeuSerArgIuLeuSmet	157
Db	499	CTTGGGCTTGTATGATGATCTACGATCTGATTTGATTCATTCATCTTGGGAAAGACCAAAATG	558
Qy	158	ArgThrTrrpIuSyrTrpGluIuhIuIuIuAlaSerLeuGluYrGlnPheAlaIasnAsp	177
Db	559	AGAGAGTGGAAAGAGTGGGAAGAGACATACAGATTCGAAATATCGATTTATTCACCGAT	618
Qy	178	ProAlaArgPheArgPheThrHisGlnIuhTrSerPheValIuSArgHisIuLeuGluLeuSer	197
Db	619	CCCGAGAGTTTAGGTTTGGCGGGATTCATCTTGGCGGAGACATCTGAGATTTCGG	678
Qy	198	SerThrProGluIuLeuArg---ThrValAlaAlaPhePheArgGlnPhePheArgSerVal	218
Db	679	AGCAATGACATATACGCTGGCTGATGTATAGTTTCTTAAGCGAGTCTTTAAATCTGTA	738
Qy	217	ThrIuSValAspTyrIuLeuThrIuLeuArgAlaIuPheIleAsnAlaHisIuLeuSerHisAsn	233
Db	739	ACCAAGTGTGATTTCTTAAACATGTAGACATAGGTTTATCATGAGCCCAATTTGGCTCGGG	798
Qy	237	Ser-----LysPheAspPheHisIuSyrTrrIleIuSArgSerMetGluAspArgPheIuys	255
Db	799	AGCGACGCAAGGTTTCGATTTCCGAAAGATATTTCCAGAGATCTTAGAGAAAGCTTCAA	858
Qy	255	ValValValGlyIleSerLeuProLeuTrpCysValAlaIleLeuThrIuPheIuAsp	274

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RESULT 3
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; Sequence 1347, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO. 1347
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1347

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111

[illegible]

TYPE: DNA
ORGANISM: Arabidopsis thaliana
us-09-938-842A-1689

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Query Match:	39.73%	Indels:	88
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US-09-857-896a-32 (1-534) x US-09-938-842A-1689 (1-1725)

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DB 148 GCTGCTGTTTACTTTCTTCTCATGCTGTTCTGTTCTGTTGAAAACCTTTCACAAA 207
OY 42 LeuGlnHisTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGlnLysIle 61
DB 208 GTTGGAAAGGTTCTATGGGATCGGCACAAAGACAGCTCTTGGACGCTTGGACAGATC 267
OY 62 LysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuAlaValThrGlnAspPro 81
DB 268 AAGGAGAGCTGATGCTTCTGGATCATCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 327
OY 82 IleSerGlyIleCysIleSerGlyLysAlaAlaSerIleMetArgProCysSerLeuPro 101
DB 328 ATTGTGGATATTGTATCCCTTTCACATGTCGTCGATGTCGCCGTGCTGCTGCTGCT 387
OY 101 ----- 101
DB 388 AACTGAAAAAGAGATGATGACATGTCGAAAGTCACAGGACACTCTGCTTTGAG 447
OY 102 -----ProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysLys 117
DB 448 CACACATTTTATATCTGGAGGTGAAGACATCTCCCACTAA-----TGACAGAGAG 498
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OY 138 LeuAlaValPheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMet 157
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OY 158 ArgThrTrpLysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAsp 177
DB 619 CCGGATGAGAGCATGCGAGAAATGAGACATCTCCATATTGACGATTTTCACAGAGAC 678
OY 178 ProAlaSerPheArgPheThrHisGlnThrSerPheValLysArgHisLeuGlyLeu--- 196
DB 679 ACTTCAAGATTCAGGCTTACCTCAAGAAACATCTTGTGTGAAGGCGCACACCATTTCTGG 738
OY 197 SerSerThrProGlyIleArgTyrPheValAlaIlePheArgGlnPhePheArgSerVal 216
DB 739 ACCCGATTCATCTTTCTTATGTTGGATGCTTTTCACAGAGTTTTCACAGTCCGTT 798
OY 217 ThrLysValAspTyrLeuThrPheArgAlaGlyPheIleAsnAlaHisLeuSerHisAsn 236
DB 799 GGGAGAGCTGATTTGACATTTGAGAAATGGTTTACAGCTGCTTCATTTAGCTCCAGGA 858
OY 237 SerLysPheAspPheHisLysTyrIleLysArgSerMetGluAspAspPheLysValAla 256
DB 859 AGTCAATTAACTTCCAAAATACATTAAAGATGCTGGAGATGATTTCAAGTAGTGC 918
OY 257 ValGlyIleSerLeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAsp 276
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OY 277 GlyIleGlyThrLeuThrTrpIleSerPheIleProLeuValIleLeuLysValGly 296
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DB 982 ACAAAAGCTTCAAGGATTTATGACAAAGATGGCTTGGTATTCACAGATGACATGCGGTA 1041
OY 317 IleLysGlyAlaProValValGluProSerAsnLysPhePheTrpPheHisArgProAsp 336
DB 1042 GTTCAAGGAATGCGCTTGTACAAAGGACAGATGATTTCTGGTTCGGCTGCCCAT 1101
OY 337 TrpValIlePhePheIleHisLeuThrPheGlnAsnAlaPheGlnMetAlaHisPhe 356
DB 1102 TTGATTCCTCATCTCAAGCATTTTCGGCTTGTTCGAAGCGCATTTTCAGATCACTTATTC 1161
OY 357 ValTrpThrValAlaThrProGlyLeuLysCysPheHisMetHisIleGlyLeuSer 376
DB 1162 TTCTGGATGATGATTTCTTGGATGATGATTTCTTGTGATCACTTAATTTCAAGATGCA 1221
OY 377 IleMetLysValValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrIleThrPhePro 396
DB 1222 CTGTAAAGATGAGGATGCTTATGAGAGATTTGTGTTCGACGATACATCACTTCTCT 1281
OY 397 LeuTyrAlaLeuValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGluGln 416
DB 1282 CTTTACGCACTCGTACTCAGATGGGTTCTCGGATGAAAATCGGATATTGATGACAA 1341
OY 417 ThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLysLysValArgAsp 436
DB 1342 ACGTCAAAAGCAGCTCAAGAAATGGAGAAATGGAGTGAAGAAAGAAAGGTGTGAAGACC 1401
OY 437 ThrAspMetLeuMetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSerPro 456
DB 1402 ACTTAAAGACATAGCT-----GGAGATGGAAGTGCAGACCTTAGCGCATGCA 1452
OY 457 MetProSerArgAlaSer-----SerProValHisLeu 467
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OY 468 LeuHisLysGlyMetGlyArgSerAspArgProGlnSerAla----- 481
DB 1513 AGATACGAAGACT-----GACCTGAAACATCGGATGTCACACAGATAT 1560
OY 482 -----ProThrSerProArgThrMetGluGlnAlaArgAspMetTyrPro 496
DB 1561 GAAGCTTTGACTCTCCAAATCTCTCCAAAGCTTCGAG----- 1599
OY 497 ValValAlaHisProValHisArgLeuAsnProAlaAspArgArgSerValSer 516
DB 1600 CTGTGTGTGAAGTGAACCAAAATTAAGACAAATACCGGCTGAGACTAGCCGT----- 1650
OY 517 SerSerAlaLeuAspIleProSerAlaAspPheSerPhe 531
DB 1651 -----GACACTGAACATGATTTCAAGAGTTCTCTTTC 1683
RESULT 5
US-09-938-842A-2268
Sequence 2268, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
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PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2268
LENGTH: 1491
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842a-2268

Alignment Scores:
Pred. No.: 1,55e-99 Length: 1491
Score: 955.00 Matches: 209
Percent Similarity: 57.09% Conservative: 85
Best Local Similarity: 40.58% Mismatches: 169
Query Match: 34.30% Indels: 52
DB: 9 Gaps: 10

US-09-857-896a-32 (1-534) x US-09-938-842a-2268 (1-1491)

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Qy 32 SerValLeuLeuGluHisAlaLeuHisLysLeuGluHisTrpPheHisLysArgHisLys 51
Db 79 TCTTTTCCGCGAGCGCTCTCATTCACGCTCGCGGAGAGCACTTTAAGAACACATCAG 138
Qy 52 AsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValGlyPheIle 71
Db 133 AAGCAGCTTTTGGGCGCATTCACAAAGATCAAAAGAGCACTTACGTCAGAGGTTTCATA 198
Qy 72 SerLeuLeuLeuAlaValAlaThrGlnAspProIleSerGlyIleCysIleSerGluLysAla 91
Db 199 TCGTTCATATTATGCGTGGCGGCGGCTCTAAATCCGAAAGATTTCATATCAAGAAGGCTTA 258
Qy 92 AlaSerIleMetArgProCysSerLeuProProGlySerValLysSerLysTrpLysAsp 111
Db 259 AGTGAAGAAGTTTCTCCCTGTACGAACCTGAGGCGCTGAAGTCC--CTTAAAGAC 315
Qy 112 Tyr----- 112
Db 316 TCCGCCATTTCCAGTTCACGCTCACCGGCGCTCATCTCGCGGAGATGCCCGCCG 375
Qy 113 -----TyrCysAlaLysLysGlyLysValSerLeuMetSerTrpGlySerLeuHisGln 130
Db 376 GGTGACTACTGCTCCCTTAAGGGAAAAAGTACCAATATGTCATATTCAGCTCGACGAG 435
Qy 131 LeuHisIlePheIlePheValLeuAlaValPheHisValThrTyrSerValIleIleMet 150
Db 436 CTTCATATATTCATCTTCGTAATAGCTGTGGCCACATTAATTTCTCGCTCTTAACCAT 495
Qy 151 AlaLeuSerArgLysLysMetArgThrTrpLysLysTrpGluThrGluThrAlaSerLeu 170
Db 496 GTTTTGGTACCATGAAGATTAAGCAATGAAAGAAAGGAGGATTAAGTT-----TTA 549
Qy 171 GluTyrGlnPheAlaAsnAspProAlaArgPheArgPheTrpHis-----GlnTrpSer 188
Db 550 GAGAAGACTTCGACACACACCAAGATATAAAGAAATACACACGCTTCAGAACACGAA 609
Qy 189 PheValLys---ArgHisLeuGlyLeu---SerSerTrpProGlyIleArgTrpValAla 206
Db 610 TTTCATCAGGTCAGATTTCTTGGGTTGGAAAAAGCTGATGCTTCCTTGGGATGGTGCA 669
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Db 670 TCGTTATGAAGAGTTTCTTGGCGTCAATGATGATGATTCATCATCAACATGAAGGCTTA 729
Qy 227 GlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLysTrpLysLys 246
Db 730 GCGTTTGACAGACTCATTCAGAACCAACCAAAATTCATTTCCATTAAGTTTAAAG 789

Qy 247 ArgSerMetGluAspAspPheLysValAlaValGlyIleSerLeuProLeuTrpCysVal 266
Db 790 CGTGCCTTAATTCGATTTTCAAGAAAGTCTGGTATACAGTGGTACCTTGGGATTT 849
Qy 267 AlaIleLeuThrLeuPheLeuAspPheLysArgLysIleGlyThrLeuThrTrpIleSerPhe 286
Db 850 GTGGTTCTCTTCTCTTCAACATTTGGATGGCATGTTTACTTCTGGCTAGGCTTT 909
Qy 287 IlePheLeuValIleLeuLeuCysValGlyThrLysLeuGluMetIleIleMetGluMet 306
Db 910 ATTCTTTATTCCTTTTACCGCTGGGAGCAAGATTATGACATATCATCACAGATTGG 969
Qy 307 AlaLeuGluIleGlnAspArgAlaSerValIleLysGlyAlaProValAlaGluProSer 326
Db 970 GCTCATGAAGTTGCAGAAACACATTCGTGTGAAGGAGATTGGTTGTCGACATCA 1029
Qy 327 AsnLysPhePheTrpPheHisArgProAspTrpValLeuPhePheHisLysThrLeu 346
Db 1030 GATGATTTGTGTGTTTCAAGTCCCGGCTAGTCTCTCTTGATCATTCATTCATT 1089
Qy 347 PheGlnAsnAlaPheGlnMetAlaHisPheValTrpValAlaThrProGlyLeuLys 366
Db 1090 TTCCAAACCTCCTTGAATGCGCTACTTCTCTTATCCCTTTTCAATTGCTGGGAT 1149
Qy 367 LysCysPheHisIleMetHisIleGlyLeuSerIleMetLysValAlaLeuGlyLeuAlaLeu 386
Db 1150 TCATGATCATGATCATGATCATGATCATGATCATGATCATGATCATGATCATGATCAT 1209
Qy 387 GlnPheLeuCysSerTrpIleThrPheProLeuTyrAlaLeuValThrGlnMetGlySer 406
Db 1210 CACCTTCTGTGACGATCACTTACGCTCTATGACCTGTGATCACTGATGAGAAAT 1269
Qy 407 AsnMetLysArgSerIlePheAspGluGlnThrAlaValAlaLeuThrAsnTrpArgAsn 426
Db 1270 TCATTAAGAGGTCAATATTCACAGACACACAGAACATCTTGGATGCCAATA 1329
Qy 427 ThrAlaLysGluLysLysValAlaArgAspThrAspMetLeuMetIleGly 446
Db 1330 ATGGCTTAAGAGGAGGTCAACAAAGGCCCAACAGTA----- 1368
Qy 447 AspAlaThrProSerArgGlyThrSerProMetProSerArgAlaSerSerProValHis 466
Db 1369 ---GATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1419
Qy 467 LeuLeuHisLysGlyMetGlyArgSerAspAspProGlnSerAlaProThrSerProArg 486
Db 1420 TTGCTAGAAAGAGGCTCTCTCAACAAATACAG-----AACCCAG 1461
Qy 487 ThrMetGluGluAlaArgAspMetLysProValAlaValAlaHis 501
Db 1462 GAAAAATCAGAG-----ATTGCTCAC 1482
RESULT 6
US-09-938-842a-1086
Sequence 1086, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krieps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379

```
; SEQ ID NO 1086
;
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1086
```

Alignment Scores:	
Pred. No.:	6,466-97
Score:	93.50
Percent Similarity:	56.19%
Best Local Similarity:	40.16%
Query Match:	33.49%
DB:	9
Length:	1581
Matches:	198
Conservative:	79
Mismatches:	167
Indels:	49
Gaps:	8

US-09-857-896A-32 (1-534) x US-09-938-842A-1086 (1-1581)

Qy	12	TLRLeuProGluThrProSerThrValAlaLeuValPheAlaValMetIleLeuVal	31
Db	25	TCGCTTGAATTCATCTGCACGAGGGGTGGCGGAGTTTGTACGGATCATCGCGGAT	84
Qy	32	SeValLeuLeuGluHisAlaLeuHisValLeuGluHisIleStrPheHisValArgHisLys	51
Db	85	TCACGTGGCGGTGACGGTTGGCTCCATATTGGTACATTTGGTCTTAAGAAGAAAGCA	144
Qy	52	AsnAlaLeuAlaGluAlaLeuGluValIleValAlaGluLeuMetLeuValGlyPheIle	71
Db	145	AAACCCCTTTACGAAACCCTTTAAAGGTTTAAAGAAAGCACTGATGTGTAGGGGTTTAA	204
Qy	72	SeLeuLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGluLysAla	91
Db	205	TGCGTGTTACGACGGATATTCAGAGGCGCATTTCCAAATCTGTGTGAAGAAATGTG	264
Qy	92	AlaSerIleLeuIleArgProCysSerLeuProGlyLys	103
Db	265	CTTATGATATGCTTCATGTTCTCTGTGATTCAGACGAGAACTGGGCGCACTGACAT	324
Qy	104	-----SerValLysSerLysTyLysAspTyr-----	112
Db	325	AAAACGTTACGCAAAACAAACATTTTCAGACTTTTTCACATTTCTTGGACACCTAGG	384
Qy	113	-----TyrCysAlaLysLysGlyLysVal	124
Db	385	CGTCTACTTGCTGACATCTGTCTGCAAGTTGGTTCCTACCGAAAGAGGTAAAGTA	444
Qy	121	SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal	140
Db	445	CCATGCTTGTGGTGAAGGCATTCAGCCATCTCAATATTTTCATCTTCGCTCGCCATA	504
Qy	141	PheHisValThrTyrSerValIleIleMetAlaLeuSerAlaGlyLeuLysMetArgThrTyr	160
Db	505	TCCCATGTGACATTTCTGTCTCTTACCGTGATTTTGGAAACGACAAAGATCCCAATGG	564
Qy	161	LysAlaIleArgLysThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAspPro-----	178
Db	565	AAAGAAATGGAGGATTCGATCCGACAAATGAAAGATT-----GACCCCAAAACA	612
Qy	179	-----AlaArgPheArgPheThrHisGlnThrSerPheValLysArgHis--	193
Db	613	GCCTCAGAGAAAGAGGCTCAGTCATGATGACAAACATCGTTTATTAAAGACATTTT	672
Qy	194	LeuGlyLeuSerSerThrProGlyLys-----ArgTyrValAlaIlePheArgGlnPhe	212
Db	673	CTTGTGATTGGCAAGATTCACATCTCCCTCGAGTGGACGCAATCTTTTTCAGCAAAATTC	732
Qy	213	PheArgSerValThrLysValAspTyrLeuThrLeuArgAlaGlyPheIleAsnIleHis	233
Db	733	TATGATTCCTGTGACGAAACAGATTAAGTACTTTACGCTTGGTTTCATTATGACACAT	792
Qy	233	LeuSerHisAsnSerThrPheAspPheHisLysTyrIleLysArgSerMetGlnAspArg	253
Db	793	TGTAAAGGAAACCCCAAGCTTAAATTTCCAAAGATATGAATGCGCGCTCAAGAGATAT	852
Qy	253	PheLysValValValGlyLysSerLeuProLeuTyrPcysValAlaIleLeuThrLeuPhe	272

Db	853	TTCAACACAGTCTTGATTAAGTGGATCTTGAGATCTTGTCGTCATCTTTGGTCG	912
Qy	273	Leuasp1LeaspG11eg1YthrLeuThrPheLeuSerPheIleProLeuValIleLeu	292
Db	913	CTAAAGTTCACGAGTGCACACATATTTCTGGATGACATTTATCTCTTGCTTGCTT	972
Qy	293	LeucysValG1YthrLysLeuGluMetIleIleMetGluMetAlaLeuGluIleGlnAsp	312
Db	973	CTTCGCTGGGACCAAGATTGGACAGCATGATATTGCACAGTATGGCTCATGAAGTTGCAG	1033
Qy	313	ArgAlaSerValIleLysGlyAlaProValAlaGluProSerAsnLysPheThrPhe	332
Db	1033	AAACAGTAGCATGAAGGAGCACTTGATGGTGAACCCCTGACATGAGCATTTCTGGTTC	1093
Qy	333	HisArgProAspTrpValLeuPhePheIleHisLeuThrLeuPheGlnAsnAlaPheGln	352
Db	1093	AGCAACGTCCAATGTTCTCTGACTATGATCATATTATGCTCTTCCAGAAATGCTTTGAG	1153
Qy	353	MetAlaHisPheValTrpThrValAlaThrProGlyLeuLysCysPheHisMetHis	372
Db	1153	ATTGCGCTTTTCTTTGGATTTGGGTTACATACGGCTTCGACGCTGATATGAGGACAG	1213
Qy	373	IleGlyLeuSerIleMetLysValValLeuGlyLeuAlaLeuGlnPheLeuCysSerTrp	392
Db	1213	GTGAGATACATGTTCCCAAGATTCGTATATGGGGCTTTCATTTCAAGTCTTTGCATGAC	1273
Qy	393	IleThrPheProLeuTrpAlaLeuValIleThrGluMetGlySerAsnMetLysArgSerIle	412
Db	1273	AGTACAGCTCCCTTTTACGGCATGCTCTCACAGATGGGAAGTACCTTCCAGAAAGCTATA	1333
Qy	413	PheAspGluGlnThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLys	432
Db	1333	TTTGAGAGAGAAATGTCAGAGTTGGTTCGTTGTTGGGCACAGAAAGTGAACAAAAGACA	1393
Qy	433	LysValArgAspThrAspMetLeuMetAlaGluMetIleGlyAspAlaThrProSerArg	452
Db	1393	-----GACCTTAAAGCTGCAGCTAGTAAATGAGACGAAGAGCTCTCAG	1433
Qy	453	--GlyThrSerProMetProSerArgAlaSerSerPro	464
Db	1438	GCTGGTCTGCTGCTGATTCGTTCTGTTCTGTTCTGCTGCTC	1476
RESULT 7			
US-09-770-445-226			
Sequence 226, Application US/09770445			
Patent No. US20020023281A1			
GENERAL INFORMATION:			
APPLICANT: Gorlach, Jörn			
APPLICANT: Ah, Yong-Qiang			
APPLICANT: Hamilton, Carol M.			
APPLICANT: Price, Jennifer L.			
APPLICANT: Raines, Tracy M.			
APPLICANT: Yu, Yang			
APPLICANT: Rameaka, Joshua G.			
APPLICANT: Page, Amy			
APPLICANT: Mathew, Abraham V.			
APPLICANT: Ledford, Brooke L.			
APPLICANT: Woessner, Jeffrey P.			
APPLICANT: Haas, William David			
APPLICANT: Garcia, Carlos A.			
APPLICANT: Krieker, MaJa			
APPLICANT: Slader, Ted			
APPLICANT: Davis, Keith R.			
APPLICANT: Allen, Keith			
APPLICANT: Hoffman, Neil			
APPLICANT: Hubban, Patrick			
TITLE OF INVENTION: Expressed Sequences of Arabidopsis			
FILE REFERENCE: 202305 (PAA-012PRV)			
CURRENT APPLICATION NUMBER: US/09/770,445			
CURRENT FILING DATE: 2001-01-26			
PRIORITY APPLICATION NUMBER: US 60/178,472			

;; PRIOR FILING DATE: 2000-01-27
;; NUMBER OF SEQ ID NOS: 999
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 226
;; LENGTH: 1007
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1007)
;; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-226

Alignment Scores:
Pred. No.: 1.04e-43 Length: 1007
Score: 465.00 Matches: 93
Percent Similarity: 60.81% Conservative: 42
Best Local Similarity: 41.89% Mismatches: 81
Query Match: 16.70% Indels: 6
DB: 10 Gaps: 2

US-09-857-896a-32 (1-534) x US-09-770-445-226 (1-1007)

Qy 244 Trrilelarsarsetmetglunaspapheulysvalvalgylileserleuproleu 263
Db 1 TATATGATGCGCGCTCTAGAGGATGATTCAACAGTGTGTGATATGATGATCTT 60
Qy 264 TTPCYsVALAlAlleuThrleupheleusplleasprlyleelythrleuthr 283
Db 61 TGGATCTTGTGTCATCTTTTGGCTGCTAAATGTAAAGGATGGCACATATTTCTGG 120
Qy 284 lIeserphelieproleuValileleuCySValglYThrlyleuglunetille 303
Db 121 ATAGCATTTATTCCTTGGCTTCTGCTGCTGCGGAACAAAGTTGGCATGTGAT 180
Qy 304 MetglumetAlaleuglulileglnasprglaserValileysglYAlarproVal 323
Db 181 GCACAGTACGTCATGAGTTCGACAGAAACATGTAGCCATTTAGAGACATTTAGTGTG 240
Qy 324 GluproseranlysphehtrpPhenIsArgproAsprTrValleupheleIs 343
Db 241 AAACCCCTGATGAGCATTTCTGCTGACAGCAACCTCAAAATGTTCTCTACATTCAT 300
Qy 344 LeuThrleupheglInasnalArPheglmetAlAnIsPheValTrPrThrValAlArhrPro 363
Db 301 TTTATCCCTTCGACAAATGCTTTTGAGATGGCTTTTCTTTGATTTGGGTACATAC 360
Qy 364 GlyleuLysCysPhehIsMethIsIleGlyleuSerIlleMetlySValValleugly 383
Db 361 GGCTTCGACCTGCTCATTTATGAGCAGGAGGAAATACATTTGTCACAGATTTGGTTACGGG 420
Qy 384 LeuAlAlaleuglnPheleuCySserTyrlleThrPheproleuThrAlaleuValThrgln 403
Db 421 GTCCTCATTTCAAGTCTTTCGACATTTACAGTACGCTGCTTTTACGCAATCGTCACAG 480
Qy 404 MetGlySeranMetlySArgserIllePheasprgluglnThrAlalaleuThrasn 423
Db 481 ATGGAGATGACCTTCAGAAAGCTATATTCCNAGGAATGACAGTTGGTGGTCTTGGT 540
Qy 424 TTPArgAsnThrAlalysglulyslySlySValArGAsprThrasPheleuMetAlagln 443
Db 541 TGGCAGACAGAAAGTGAACAAAGAGA-----GACCTAAAGAGCTGAGCT 585
Qy 444 MetIleGlyAspAlarhrProserArg---GlyThrSerProMetProserArgAlaser 462
Db 586 AGTAATGGAAAGAAAGAGACGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
Qy 463 SerPro 464
Db 646 GCTCCT 651
RESULT 8
US-09-770-444-164

;; Sequence 164, Application US/09770444
;; Patent No. US20020023280A1

;; GENERAL INFORMATION:
;; APPLICANT: Gorlach, Jorn

;; APPLICANT: An, Yong-Qiang

;; APPLICANT: Hamilton, Carol M.

;; APPLICANT: Price, Jennifer L.

;; APPLICANT: Raines, Tracy M.

;; APPLICANT: Yu, Yang

;; APPLICANT: Ramakea, Joshua G.

;; APPLICANT: Page, Amy

;; APPLICANT: Mathew, Abraham V.

;; APPLICANT: Ledford, Brooke L.

;; APPLICANT: Woessner, Jeffrey P.

;; APPLICANT: Haas, William David

;; APPLICANT: Garcia, Carlos A.

;; APPLICANT: Krickler, Maja

;; APPLICANT: Slader, Ted

;; APPLICANT: Davis, Keith R.

;; APPLICANT: Allen, Keith

;; APPLICANT: Hoffman, Neil

;; APPLICANT: Hurdan, Patrick

;; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

;; FILE REFERENCE: 2027 (PARA-016PRV)

;; CURRENT APPLICATION NUMBER: US/09/770,444

;; PRIOR FILING DATE: 2001-01-26

;; PRIOR APPLICATION NUMBER: 60/178,502

;; NUMBER OF SEQ ID NOS: 999

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 164

;; LENGTH: 471

;; TYPE: DNA

;; ORGANISM: Arabidopsis thaliana

;; FEATURE:
;; NAME/KEY: misc_feature

;; LOCATION: (1)...(471)

;; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-164

Alignment Scores:

Pred. No.: 2.97e-42 Length: 471
Score: 447.50 Matches: 88
Percent Similarity: 70.06% Conservative: 22
Best Local Similarity: 56.05% Mismatches: 44
Query Match: 16.07% Indels: 3
DB: 10 Gaps: 2

US-09-857-896a-32 (1-534) x US-09-770-444-164 (1-471)

Qy 157 MetArgThrTrpLysLeuTrpGluThrGluThrAlaserleuGluTyrglnPheAlaasn 176
Db 1 ATGAGCGATGGAGATCGTGGGAGAGAAACAAATAGATATGATATTCACAC 60
Qy 177 AsprProAlArGPharGPhethrhnIsGlnThSerPheValLyArgnIsleuGlyleu 196
Db 61 GATCCTGAGATGAGTTCGAGGACATCTTTGGAGAAACATCTCAATTTC 120
Qy 197 ---SerSerThrProGlylleArgTrpValAlAlArPheArGlnPheArGser 215
Db 121 TGGAGCAGACAGAGAGTGCACACTATGATGTTGTTTATAGACATCTTGTGATCT 180
Qy 216 ValThrLysValAsprTyLeuThrleuArgAlGlyPheIlleAsnAlAnIsleuSer--- 234
Db 181 GTACCCAAATGGATTACTTAgCAGTACATGATGTTTCATGATGCGCATTTTGGCTCC 240
Qy 235 ---HisAsnSerLysPheAspPhehIsLysTyrlleYsArgSerMetGluAspPhe 253
Db 241 GGTACAGAAATCAAGATTCGATTTCCGCAAGATATACAGAGATCATTTAGAAAGACTTC 300
Qy 254 LysValAlValAlGlylIleSerleuProleuTrpCySValAlAlIleleuThrleuPheleu 273
Db 111 111111 111111 ::::111 111

Db 301 AAAACGTTGTGAATCAGTCGCTTATCTGTTNNNNCTGTGCTATTCCTTGACC 360
Qy 274 AsplleapgllyleaglYthrleuthrtriplleserphelileproleuvalileleu 293
Db 361 AATTCATATGATGATACGTTCTTACCTGGTACATTCATTCAGTGTGTAATCTA 420
Qy 294 CysValglYthrlyleuGlumetleilemetGlumetalaleuGlulle 310
Db 421 ATAGTTGGAACAAGCTTGAAAGTCATATTAACAATAATGTGCTTAAGATC 471

RESULT 9

US-09-770-444-733/C
; Sequence 733, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Kameoka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 733
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-733

Alignment Scores:

Pred. No.: 1e-30 Length: 448
Score: 346.50 Matches: 68
Percent Similarity: 66.22% Conservative: 30
Best Local Similarity: 45.95% Mismatches: 45
Query Match: 12.45% Indels: 5
Gaps: 2

US-09-857-896a-32 (1-534) x US-09-770-444-733 (1-448)

Qy 320 AlaProvalValgluProserAsnlysrphethrphelHsAspProAspTryValleu 339
Db 444 GCGCGCGAGGTACAAAGCAAGATGATTTGTGGTGGCGGCCCATTTGATTC 385
Qy 340 PhepheleHsleuThrleuPheglAsnAlaPheglMetAlaHsPheValTrpThr 359
Db 384 CATCTCATGCTATTCGCTTGTTCAGAACGCAATTCAGATCATCTTATCTTGATA 325
Qy 360 ValAlaThrProglYleuLylyscysPheHsMetHsileglYleuSerilemetlys 379
Db 324 TGGTATTCCTTTGGATGATGATTCCTGTCACATTCATTCAGATTCGATTAATA 265
Qy 380 ValValleuGlYleuAlaLeuGlInPheLeuCysserYrileThrPheProleuYrAla 399

Db 264 CTAGCGATTGCTTAGAGATATTGCTCTTTCAGCTACATACACTTCTCTTTACGCA 205
Qy 400 LeuValThrInMetGlySerAsnMetlysrArgserillepheaspGlInThrAlaYs 419
Db 204 CTCGTACTCAGATGAGGTCTTCGAGAAATAATGATTCATGCATGACAAACGTCAAA 145
Qy 420 AlaLeuThrAsnTrpAAsnThrAlaYsGlYlysrlysrValArGAspThrAspMet 439
Db 144 GCACCTCAGAAATGGAATGCAATGCGAGGAAGAAAGAAAGGTGGAAGCCACTTAAG 85
Qy 440 LeuMetAlaGlInMetileglYAspAlaThrProser-----ArgglYThrSer 455
Db 84 AGACTAGGTGGA--GATGGAAGTGGAGCCCTACGCGCATGACAGATTAAGTCTACTTG 28
Qy 456 PrometProserArGAlaSerSer 463
Db 27 TCTGTACTGCGCGCGCGCGCT 4

RESULT 10

US-09-878-574-1249
; Sequence 1249, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Ia Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1249
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-040-Q1-B1-A8
US-09-878-574-1249

Alignment Scores:

Pred. No.: 7.7e-30 Length: 396
Score: 338.00 Matches: 64
Percent Similarity: 69.17% Conservative: 19
Best Local Similarity: 53.33% Mismatches: 35
Query Match: 12.14% Indels: 2
Gaps: 1

US-09-857-896a-32 (1-534) x US-09-878-574-1249 (1-396)

Qy 316 ValileysglYAlaProvalValgluProserAsnlysrphethrphelHsArgPro 335
Db 9 GTGGTCAAGGCTGACCTTGTGTTGAGCAGCAAGATGAATGTTCTGTTCAATGACACC 68
Qy 336 AspTrpValleuPhepheleHsleuThrleuPheglAsnAlaPheglInMetAlaHs 355
Db 69 CGCCCTACATCCCTTTTGTGATCATCTGTCTCTTTCAGAAATGATTCATACAGCTTT 128
Qy 356 PheValThrPheValAlaThrProglYleuYs-----LysCysPheHsMetHsile 373
Db 129 TTTGGTTCAGACCATATGCAATGGGTTCAAAATTAACCTGTTTCCACAAACTACT 188
Qy 374 GlyleuSerilemetlysrValleuGlYleuAlaLeuGlInPheLeuCysserYrile 393
Db 189 GCAGATATTCATATGACTTTCATCATATGGGGTTCTCACAAATTCATATGAGTATG 248
Qy 394 ThrPheProleuYrAlaLeuValThrInMetGlySerAsnMetlysrArgserillephe 413
Db 249 ACTTGGCTCTTGAAGCTCTAGTACACCAAGTGGCTTCTACATGGAACCTATTTTTC 308
Qy 414 AspGlInThrAlaYsAlaLeuThrAsnTrpAAsnThrAlaYsGlYlysrlysr 433

Db 309 AATGAATGTTCAGTACGCTGAAAGAACTGCATCATCTGCTAAAGACATCAAA 368

RESULT 11

US-09-878-574-13167
Sequence 13167, Application US/09878574
Patent No. US2002010548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEO ID NO 13167
LENGTH: 279
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701066723H1
US-09-878-574-13167

Alignment Scores:

Pred. No.:	1,23e-16	Length:	279
Score:	220.50	Matches:	39
Percent Similarity:	66.67%	Conservative:	23
Best Local Similarity:	41.94%	Mismatches:	30
Query Match:	7.92%	Indels:	1
DB:	10	Gaps:	1

US-09-857-896a-32 (1-534) x US-09-878-574-13167 (1-279)

Oy 206 ValAlaPhePheArgGlnPhePheArgSerValThrLysValAlaPtyrLeuThrLeuArg 225

Db 4 CTAATGTTACAGCCCAATTTTGGACTTCCACACAGAGCTGATTTCATGAGATTGGCC 63

Oy 226 AlaGlyPheIleAsnAlaHisLeuSerHisAsnSerLysPheAspPheHisLysTyrIle 245

Db 64 TTAGCTTCATTACTTAATCAT--GGTCTTCCACACATCATGACGCTCCACACATATATG 120

Oy 246 LysArgSerMetGluAspAspPheLysValValGlyIleSerLeuProLeuTyrPys 265

Db 121 CTTCCAGACATGATGAGCAATTCGTGACATAGTGTGTTAGTGTCTCTCTGGTA 180

Oy 266 ValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThrLeuThrTyrIleSer 285

Db 181 TATGCCATCTCTGTATTCTTAATTTTTCACGAGCAACTTTTACTTCTGGCTGTC 240

Oy 286 PheIleProLeuValIleLeuLeuCysValGlyThrLys 298

Db 241 TTCGTTCCAGCAATTTGATCTTATCATCTGATGACTTAA 279

RESULT 12

US-09-924-035A-887/C
Sequence 887, Application US/09924035A
Patent No. US20020142319A1

GENERAL INFORMATION:

APPLICANT: Griach, Jrn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,784
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSeq for Windows Version 3.0
SEO ID NO 887
LENGTH: 455
TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(455)

OTHER INFORMATION: n = A,T,C or G

US-09-924-035A-887

Alignment Scores:

Pred. No.:	3.04e-09	Length:	455
Score:	159.00	Matches:	30
Percent Similarity:	79.07%	Conservative:	4
Best Local Similarity:	69.77%	Mismatches:	9
Query Match:	5.71%	Indels:	0
DB:	10	Gaps:	0

US-09-857-896a-32 (1-534) x US-09-924-035A-887 (1-455)

Oy 390 CysSerTyrIleThrPheProLeuTyrAlaLeuValThrGlnMetGlySerAsnMetLys 409

Db 453 TGCAGCTACATCATCTCTCCATTTGTAGCCCTGTTACTACATGATGGTTACACATGAAG 394

Oy 410 ArgSerIlePheAspGlnThrAlaLysAlaLeuThrAsnTyrArgAsnThrAlaLys 429

Db 393 AAACAGATGTTGATGAGCAAAATGCAAGGAGCATGAGAGAGTGCCACAAAGACATCA 334

Oy 430 GluLysLys 432

Db 333 TTGAAGAA 325

RESULT 13

US-09-770-444-512/C

Sequence 512, Application US/09770444

Patent No. US2002023280A1

GENERAL INFORMATION:

APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Olang
APPLICANT: Hamilton, Carol M.
APPLICANT: Princes, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEO ID NO 512
LENGTH: 457
TYPE: DNA
ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(457)

OTHER INFORMATION: n = A,T,C or G

US-09-770-444-512

Alignment Scores:

Pred. No.: 3,06e-09 Length: 457
Score: 159.00 Matches: 30
Percent Similarity: 79.07% Conservative: 4
Best Local Similarity: 69.77% Mismatches: 9
Query Match: 5,71% Indels: 0
DB: 10 Gaps: 0

US-09-857-896a-32 (1-534) x US-09-770-444-512 (1-457)

OY 390 CysSerTrpIleThrPheProLeuAlaLeuValThrGluMetGlySerAsnMetLys 409
Db 455 TGCAGCTACATCATCTCTCCATGTAGCCCTGCTACTGATGAGTGGTACACATGAAG 396
OY 410 ArgSerIlePheAspGluGlnThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLys 429
Db 395 AAAGCAGCTGTGGATGACCAATGCAAAAGCATGTGAAGAAGTGCACAAAGACATCAAA 336
OY 430 GluLysLys 432
Db 335 TTGAAGAAA 327

RESULT 14

US-09-923-876-2134
; Sequence 2134, Application US/05923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalquidi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 2134
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700160106H1
; US-09-923-876-2134

Alignment Scores:

Pred. No.: 1,12e-07 Length: 268
Score: 142.00 Matches: 26
Percent Similarity: 58.62% Conservative: 14
Best Local Similarity: 58.24% Mismatches: 28
Query Match: 5,10% Indels: 0
DB: 10 Gaps: 0

US-09-857-896a-32 (1-534) x US-09-923-876-2134 (1-268)

OY 330 PheTrpPheHisArgProAspTrpValLeuPhePheHisLeuThrLeuPheGlnAsn 349
Db 62 TTTTGGTTGGAAAGCCCTCGGGTACTGTGGCTTATACAGTTCATTTCATTTCAGAAAT 121
OY 350 AlaPheGluMetAlaHisPheValTrpThrValAlaThrProGlyLeuLysCysPhe 369
Db 122 GCTTTGACCTGGCAGCATCTTATGGTCTGTGGAGACTGAGTGCACATACATGTTTG 181
OY 370 HisMetHisIleGlyLeuSerIleMetLysValAlaLeuGlyLeuAlaLeuGlnPheLeu 389
Db 182 ATGAGCACTACTACATGTTGGCATTCGGTTCATTTTCGGGCTCTAGTACAGTTTGG 241

OY 390 CysSerTrpIleThrPheProLeu 397
Db 242 TGCAGCTACAGCACATGCGCTG 265

RESULT 15

US-10-032-717-9
; Sequence 9, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins with
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; OTHER INFORMATION: Make optimized Cry1218-1
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: mol218-1

US-10-032-717-9

Alignment Scores:

Pred. No.: 0.0246 Length: 2010
Score: 108.00 Matches: 46
Percent Similarity: 40.49% Conservative: 20
Best Local Similarity: 28.22% Mismatches: 50
Query Match: 3,88% Indels: 48
DB: 12 Gaps: 7

US-09-857-896a-32 (1-534) x US-10-032-717-9 (1-2010)

OY 363 ProGlyLeuLysCysPheHisMetHis-IleGlyLeuSerIleMetLysValValLe 382
Db 198 CCAGAGCCGCCCAAGGCCGCCATGACATGCTGGCC-----AAGCTCTCTC 245
OY 382 uGlyLeuAlaLeuGlnPheLeuCysSerTrpIleThrPheProLeuTrpAlaLeuValTh 402
Db 246 CGGCTCGCGCTGCTGCTGCTG-----GCCCCCATGTCCTCTACAC 290
OY 402 rGlnMet-----GlySerAsnMetLysArgSerIlePheAspG1 415
Db 291 CCAGCTCATGACATCCTCTGGCCCTCGGCGGAGAGATGCCAAGTGGGAATGTCATGGA 350
OY 415 uGlnThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLysValAlr 435
Db 351 GCGAG----- 354
OY 435 gAspThrAspMetLeuMetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSe 455
Db 355 -----GTGAGGAGGCTCATACACAGAGATGCGGAGTA-CGCCCCCAACAAAGGC----- 404
OY 455 rPheMetProSerArgAlaSerSerProValHisLeuLeu-----HisLysG1 471
Db 405 -----CCTTCGAGACTGGAGGCTCGGCAACAACTCCAGCTCTACCTACCGCC 457
OY 471 yMetGlyArgSerAspAspProGlnSerAlaProThrSerProArgThrMetGluGluAl 491

Db 458 TGGAGAGTGGAGAGAGACCCAGCGGCTCCCGCCCTCCGGAGCTGGCGAACCGCT 517
Qy 491 aArgAspMetIyProValValAlaHisProValHisArgLeuAsnProAlaAspAr 511
Db 518 TCGAGAT-----CCTCGACTCCCTCTTCACCCAGTACATGCTCCTCTCCGGGTGACCA 571
Qy 511 gArgArg 513
Db 572 ACTTCGA 578

Search completed: November 18, 2002, 18:08:40
Job time : 75 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 15:35:13 ; Search time 43 Seconds
(without alignments)
1193.855 Million cell updates/sec

Title: US-09-857-896A-32

Perfect score: 2784
Sequence: 1 MAEDYEPPPARTLPETPSMA.....VSSGALDADIPSADEFSFSG 534

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2434	87.4	533	T04481	Mlo protein - barley
2	1960	70.4	544	T05952	Mlo-hn protein - b
3	1762	63.3	537	T03797	probable mlo prote
4	1276.5	45.9	573	B86247	hypothetical prote
5	1246.5	44.8	570	T02582	H. vulgare Mlo pro
6	1241	44.6	583	H96640	hypothetical prote
7	1119	40.2	501	B84748	similar to Mlo pro
8	1106	39.7	574	F84552	similar to Mlo pro
9	1068	38.4	580	B84552	hypothetical prote
10	1058	38.0	443	E96495	hypothetical prote
11	955	34.3	496	T00681	H. vulgare Mlo pro
12	932.5	33.5	526	T01089	hypothetical prote
13	860.5	30.9	429	T09888	hypothetical prote
14	838.5	30.1	485	T47469	hypothetical prote
15	641.5	23.0	507	H86393	protein T24P13.8 [
16	496	17.8	447	A86244	Barley Mlo protein
17	117.5	4.2	970	F64230	spore germination
18	107.5	3.9	167	C81358	probable integral
19	107	3.8	628	AG1469	transporter homolo
20	101	3.6	574	B91159	probable transport
21	101	3.6	574	B86005	probable transport
22	98	3.5	353	JC2492	G protein-coupled
23	98	3.5	574	E65135	hypothetical 64.6K
24	97	3.5	628	AF1108	transporter homolo
25	97	3.5	862	T40934	probable integral
26	97	3.5	1275	JU0092	trp protein - frui
27	97	3.5	2326	B47447	calcium channel pr
28	95.5	3.4	2108	S72458	sodium channel pro
29	95.5	3.4	770	G90506	conserved hypothet

30	95	3.4	260	2	C97003	ABC-type spermidin
31	94.5	3.4	475	2	G89587	protein R99P10.4 [
32	94.5	3.4	489	2	B33416	nuclear factor 1 -
33	94.5	3.4	499	2	S01038	transcription fact
34	94.5	3.4	506	2	A33416	nuclear factor 1 -
35	94.5	3.4	510	2	E71695	hypothetical prote
36	94.5	3.4	1274	2	JN0015	trp protein - frui
37	93.5	3.4	595	2	E64460	hypothetical prote
38	93	3.3	508	2	A89817	hypothetical prote
39	92.5	3.3	485	2	T35663	probable transmem
40	92	3.3	641	2	AG2164	hypothetical prote
41	91.5	3.3	355	2	A55733	G protein-coupled
42	91.5	3.3	432	2	F71152	probable lipopolys
43	91	3.3	444	2	T24844	hypothetical prote
44	90.5	3.3	404	2	H81699	conserved hypothet
45	90.5	3.3	510	2	T13882	cytochrome-c oxida

ALIGNMENTS

RESULT 1

T04481
Mlo protein - barley
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_rev1sion 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: T04481
R:Panstruga, R.; Buschges, R.; Piffanelli, P.; Schulze-Isfet, P.
Nucleic Acids Res. 26, 1056-1062, 1998
A:Title: A contiguous 60kb genomic stretch from barley reveals molecular evidence
A:Reference number: 215372; MUID:98128007; PMID:9461468
A:Accession: T04481
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-533 <PAM>
A:Cross-references: EMBL:Y14573; NID:92894376; PTDN:CAA74909.1; PTD:92894377
A:Experimental source: cv. Ingrid
A:Gene: MLO
A:Map position: 4
A:Introns: 43/3; 116/3; 155/3; 176/1; 204/3; 229/3; 259/2; 276/1; 289/3; 359/3; 40
C:Superfamily: barley pathogen resistance protein MLO

Query Match	87.4%	Score 2434;	DB 2;	Length 533;
Best Local Similarity	89.28;	Pred. No. 2,5e-204;		
Matches 471;	Conservative 20;	Mismatches 33;	Indels 4;	Gaps 3;
QY	9	PARTLPEPPSNVALVFAVMIIYSVLLLEHALKLGHWFKRHKRNALAELEKIKAEIMLV	68	
DB	8	PARLEPEPPSNVAVFAVMIVSVLMEHGLKLGHWFOHRRKKALMEALEKKAEIMLV	67	
QY	69	GFISLLAVTQDP--ISGICISSEKASIMRPGSL--PPGSVSKKYDYCAKKGVSLSMNG	126	
DB	68	GFISLLAVTQDPITAKICISEDAVDMPCRGEGPSKRYDY--CPGSGVVALMSG	125	
QY	127	SLHQLHIFELVLAFFHVTYSVITMALSRLKMTKRWKETETASLEYOFANDPARFRFTQ	186	
DB	126	SLHQLHIFELVLAFFHVTYSVITMALSRLKMTKRWKETETTSLEYOFANDPARFRFTQ	185	
QY	187	TSYVVRHNGISSTFGIRVVAFVFPFQFSTVVDVLTLRAGFIANHSKNSKDPKRYTK	246	
DB	186	TSYVVRHNGISSTFGIRVVAFVFPFQFSTVVDVLTLRAGFIANHSKNSKDPKRYTK	245	
QY	247	RSKEDDFKVVVGIISPLMCVAILTFLFDIDIGITLWISFTPLVILLCTGCTKLEIMEM	306	
DB	246	RSKEDDFKVVVGIISPLMGVAILTFLFDINGVGTLIWISFTPLVILLCTGCTKLEIMEM	305	
QY	307	ALEIODRASVTKGAPVPEPSNKFPMFHRPDWLFPTHLTLPQNAFOAHFVWVATPGIK	366	
DB	306	ALEIODRASVTKGAPVPEPSNKFPMFHRPDWLFPTHLTLPQNAFOAHFVWVATPGIK	365	
QY	367	KCFHHIGISLMKVVLGIALQFLCSYITPEPLVALYQNSNMKRSIFDEQTAALTNMN	426	
DB	367	KCFHHIGISLMKVVLGIALQFLCSYITPEPLVALYQNSNMKRSIFDEQTAALTNMN	426	

Db 366 KCHNQIGLSIMKVVYVGLAQLFCLSYWTFPLALYVQMGSMKKRSIFDEQTSKALINMN 425
Qy 427 TAKEKKVDPDMLMAQIGDAPTRSGTSMPSRASSPYHLHLHGKGRSDDPASAPTSR 486
Db 426 TAKEKKVDPDMLMAQIGDAPTRSGTSMPSRASSPYHLHLHGKGRSDDPASAPTSR 485
Qy 487 TMEARDMTPVVAHPVHRLNPDARRSVSSALDADIPSDAFSFG 534
Db 486 TQGEARDMTPVVAHPVHRLNPDARRSVSSALDADIPSDAFSFG 533

RESULT 2

T05952
Mlo-h1 protein - barley
C:Species: Hordeum vulgare (barley)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
C:Accession: T05952
R:Panstruga, R.
Submitted to the EMBL Data Library, May 1997
A:Reference number: Z15093
A:Accession: T05952
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-544 <PAN>
A:Cross-references: EMBL:Z95496; PIDN:CAB08860.1
C:Genetics:
A:Experimental source: cv. Igr1
A:Gene: Mlo-h1
A:Map position: 4H
A:Introns: 41/3; 139/3; 178/3; 199/1; 282/2; 299/1; 312/3; 382/3
C:Superfamily: barley pathogen resistance protein Mlo

Query Match 70.4%; Score 1960; DB 2; Length 544;
Best Local Similarity 70.6%; Pred. No. 6.1e-163;

Matches 386; Conservative 40; Mismatches 83; Indels 38; Gaps 3;

Qy 11 RTLPERPMAVAVLAVAVVITVSVLEHALKLGHPHKKHKNALAELETKAKELMGF 70
Db 8 RELSDPTMAVAVCAVAVLAVSVAMEHALKLGHPHKKHKNALAELETKAKELMGF 67
Qy 71 ISLLAVTODPISGICISEKASIMRPSCLPSPGVSKYKYD----- 113
Db 68 ISLLIVTODPVSRICTISKEGEMLPCKPYDAGCGKGNHRLMLQGESETHREL 127
Qy 114 -----CAKKGVLSMTSGSLHOLHIFPVLAHPHTVSVIIMALSRLKMTKKWFT 165
Db 128 AAPAGVDCAKOGKVALMSAGSMHQLHIFVLAHPHTVSVIIMALSRLKMTKKWFT 187
Qy 166 ETASLEYOPANDPARFRFTQTSFVKRHLGLSTPGIRMVVAFTROFFRSVTKVDYLTLR 225
Db 188 ETASLEYOPANDPSRCRFTHOTTLVRRHLGLSTPGVVMVVAFFROFFTSVTKVDYLTLR 247
Qy 226 AGFINAHLHNSGKRFPHKTYIKRSMEDPFKVVVGISLPLCVAILTLFLDIDIGITLWIS 285
Db 248 GGRINAHLSGKRRDFPHKTYIKRSLDEDFKVVYVRISLKLPAVALILFLDIDIGITLWIS 307
Qy 286 FLPVLVLLCGTKLEIMEMALEIODRASVIKGAHVPEPSNKEFWHRPDWVLEFIHLT 345
Db 308 VPLVLTLLWGTGKLEMYIMEAOEIHRESVYVGAHVEPSNKEFWHRPDWVLEFIHLT 367
Qy 346 LFOAFAOMAHFWTAAPRGKLCFPHHIGLSIMKVVYVGLAQLFCLSYTTPPLALYVQMG 405
Db 368 LFOAFAOMAHFWTAATPGKLCCKHEKMASTAKVYLVGAOILCSTITTPPLALYVQMG 427
Qy 406 SNNKRSIFDEQTAALTNMRNTAKKKKVVDTMLMAQIGDAPTRSGTSMPSRASSPV 465
Db 428 SHMKRSIFDEQTAALTNMRNTAKKKKARDAMLMAQMGGATPSV-----SSPV 479
Qy 466 HLHGKGRSDDPASAPTSRPTMEARDMTPVVAHPVHRLNPDARRSVSSALDADIP 525
Db 480 HLHGKGRSDDPASAPTSRPAEKEGG-----VQHPARKVPCDGMKRSFALDADIP 534
Qy 526 SADFSFS 532
,

Db 535 GADFGFS 541

RESULT 3

T03797
probable mlo protein - rice

C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: T03797
R:Panstruga, R.
Submitted to the EMBL Data Library, May 1997
A:Reference number: Z15093
A:Accession: T03797
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-537 <PAN>
A:Cross-references: EMBL:Z95353; PIDN:CAB08860.1
C:Genetics:
A:Experimental source: isolate IR-BB21
A:Gene: Mlo-h1
A:Introns: 42/3; 124/3; 163/3; 184/1; 213/3; 238/3; 268/2; 285/1; 298/3; 356/3; 368/3
C:Superfamily: barley pathogen resistance protein Mlo

Query Match 63.3%; Score 1762; DB 2; Length 537;
Best Local Similarity 66.2%; Pred. No. 1.2e-145;

Matches 358; Conservative 56; Mismatches 95; Indels 32; Gaps 10;

Qy 10 ARTLPERPMAVAVLAVAVVITVSVLEHALKLGHPHKKHKNALAELETKAKELMGF 69
Db 8 SRELPTPMAVAVCAVAVLAVSVAMEHGLHNL-----HKTAVLELIFVLSALAEMLLG 64
Qy 70 FISLLAVTODPISGICISEKASIMRPSCLPSPGVSKYKYD-----YYCAK-R 117
Db 65 FISLLVNAQAPISKICIPKSAANTILPCKAGQADIEEASGSRSLAGAGGDCSKFD 124
Qy 118 GKVLMSGSLHOLHIFPVLAHPHTVSVIIMALSRLKMTKKWFTETASLEYOPAND 177
Db 125 GKVALMSAKSMHQLHIFVLAHPHTVCIITGKLGRLKMKKKWESQTSLEYOPAND 184
Qy 178 PARFRFTQTSFVKRHLG--LSSTPGIRMVVAFFROFFRSVTKVDYLTLRAGEFINAHLSHN 236
Db 185 PSRRFRFTQTSFVKRHLGSFSSSTPGIRMTVAFFROFFGSVTKVDYLTMROGFINAHLSON 244
Qy 237 SKDPFHKTYIKRSMEDPFKVVVGISLPLCVAILTLFLDIDIGITLWISFPLVILLCVG 296
Db 245 SKDPFHKTYIKRSLDEDFKVVYVGLFVGLVFLDIDIGITLWISFPLVILLCVG 304
Qy 297 TKLEIMEMALEIODRASVIKGAHVPEPSNKEFWHRPDWVLEFIHLTFOAFAOMAHF 356
Db 305 TKLEIMEMAEIOIRATVIGADHVPEPSNKEFWHRPDWVLEFIHLTFOAFAOMAHF 364
Qy 357 VMTVAAPRGKLCCKFPHHIGLSIMKVVYVGLAQLFCLSYTTPPLALYVQMGSMKKRSIFDEQ 416
Db 365 VMTVAATPGKLCCKHENIMSLVEVYVGLSLOVLCSTITTPPLALYVQMGSMKKRTIFDEQ 424
Qy 417 TAKALTNMRNTAKKKKVVDTMLMAQIGD-ATPSRGTSMPSRASSPVHLHLHGKGRS 475
Db 425 TMMKLMRRKRAEKKKVADADAFLAQMSVDFATPA-----SSRSASVHLLDHRRARS 478
Qy 476 DDPOSAPT--SPRTMEARDMTPVVAHPVHRL--NPADARRSVSSALDADIPADFSF 531
Db 479 DDPSPTTVASPPAPE--DMTPVPAALASQQLDDPPDRKMASS--ADIDSDPSF 533
Qy 532 S 532
Db 534 S 534
RESULT 4
B6247
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C:Accession: BB65247
R:Thelodopsis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzbeg, S.L.; Schwartz, J.R.; Shum, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: AB6441; MID:21016719; PMID:11130712
A:Accession: BB6247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <STO>
A:Cross-references: GB:AE005172; NID:95734726; PIDN:AD49991.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: barley pathogen resistance protein MLO

Query Match 45.9%; Score 1276.5; DB 2; Length 573;
Best Local Similarity 48.8%; Pred. No. 3e-103;
Matches 251; Conservative 76; Mismatches 142; Indels 45; Gaps 4;

QY 11 RTLPETPSMAVALVFAVMIVTVSVLLEHALHLKLGHHFHRKRNALAELEKIKALMLVGF 70
DB 8 RTLEETSTMAVAVVCFLFLFISTYLEHSHIKIGTWFKKKHQAFLAELEKAKELMLLGF 67
QY 71 ISLLAATVODPISGICISEKAASIMRCSLPGSVSKYKDY----- 112
DB 68 ISLLLTIGQPPISNICISKVASTMHGCSAADEAKKYGKADGDDGDKPQRLLLE 127
QY 113 -----YCAKKKGVSLSMTSGSLDHLHIFIVLAVFHYTVSYIIMLSRL 155
DB 128 LAESTYHRRSLATKGDYCKAEKKAFAVSAYGICHLHIFIVLAVHVCYIYVAGTK 187
QY 156 KMRFTWKMETETASLEYOFANDPAREFTHQTSFVKRHLGL-SSTPGIRWVVAFFROFR 214
DB 188 KMRFTWKMEETETKTIIEYOYSDNDEPRFARDTSPFORHLNFWMSKTRVLTWVCFEFOFG 247
QY 215 SVTVVDVLTTRAGFINAHLNLS--HNSKFDYKRYIKRSMDDPRVVVGVSTPLMCVAITLTF 272
DB 248 SVTKVDYALRHRGFIAMHAFPGNESRDFRKTIQSLERKDKTYVEISPVYIMFAVYFL 307
QY 273 LDIDIGITLWISFIRPVYILLCGTLEMTIMEALTEQDASVYIKGAPVDESKNFEMF 332
DB 308 TNSGLGSLYMLPRTPVYVLLVITGKLEVIITKGLRIQEGGDVRAAPVQPDDELFWF 367
QY 333 HRPDVWLFELHLLTFONARQMAHFVWTVATPGLKCFMHNIGLSIMKVLVGLALQFLCSY 392
DB 368 GKPRFIFILHLVLEFNALQAFFAWSTYEFLNLCNCFESTADVIVILVYGAVVQLCSY 427
QY 393 ITFPLVLAIVQMSNNKRSIFDEQTAKALTNNRNARFKKKVRRDTDLMLQMGDAPPSR 452
DB 428 VTLPLVLAIVQMSKKKPYVENDRAVATALKKHNHAKETK-----HGHSGSNTPPS 480
QY 453 GTSMPBRASSPVHLHLHKGKSGSDPQSAPTSPR 486
DB 481 SRPTPTPHGSSPIHLHLNFNFNNSVENYSPSPSR 514

RESULT 5
T02582
H.vulgaris Mlo protein homolog (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 15-Jun-2001
C:Accession: T02582; D04814
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A:Reference number: Z14679

A:Accession:002582
A:Status:translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues:1-570 <R0U>
A:Cross-references: EMBL:AC004697; NID:g3402671; PID:g3402694
A:Experimental source: cultivar Columbia
Riln, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentolite, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallent, D.; Nleman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ven
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84814
A:Status: Preliminary
A:Molecule type: DNA
A:Residues:1-570 <STO>
A:Cross-references: GB:AE002093; NID:g3402694; PID:AAC28997.1; GSPDB:GN00139
A:Gene: AT2G39200; T16B24.16
A:Map position: 2
A:Introns: 39/3; 59/1; 140/3; 179/3; 200/1; 229/3; 248/3; 280/2; 297/1; 310/3; 368
C:Superfamily: barley pathogen resistance protein M10

Query Match 44.8%; Score 1246.5; DB 2; Length 570;
Best Local Similarity 45.7%; Pred. No. 1.3e-100;
Matches 257; Conservative 86; Mismatches 156; Indels 63; Gaps 11;

OY 11 RTLETPSMVAALVFVMTIVSVLLEHAHKGHMFHRRKRNLAELAETKIKAEMLVGF 70
DB 6 RSLDEPTMAVAVVCVLLFLISIMEYFLHGHMFKKKKHKLSEAEKVAEMLLGF 65
OY 71 ISLLAAYOPDISGICISERKASIMRCSLPGSVKSKY-KDY----- 113
DB 66 ISLLAVLQTPVSEICIPRNIAATWHPCS--NHOEIAKGDYIDDKRLIEDFDSNDY 123
OY 114 -----CAKKGVSIMSTGSLHDLHIFVLAAYFHYTVSYIIMASRLKMTW 160
DB 124 SPRRNLTAKGYDCAERKGVAVLSAYGHIHIFELVLAAPHYLVCITAYALGKTMMKK 183
OY 161 KKEETETASLEVOFANDPARFRFTGTSFVKRHGL-SPTPGIRWVAFAFPDFRSYTV 219
DB 184 KSMRETKTEIEGYADPERFRARDTSEGRHNLIMSKSTFLMT-----FFGSYKV 237
OY 220 DYLTLRAGFINALLHNS--KDFEKYTKRSMEDDEKVVYGVISLPLCAVALTLFLDIDG 277
DB 238 DYLTLRAGFINALLHNS--KDFEKYTKRSMEDDEKVVYGVISLPLCAVALTLFLDIDG 297
OY 278 IGLTWTWISFTVILLICVGTKEIMIMALEIODRASVYKGAVPVPSKKEFHWPRDM 337
DB 298 WDSYLMPLPRLIVILIVYAKLQIMTSKGLRIQEKGDVYKGAVPVPSKKEFHWPRDM 357
OY 338 VLPEFHLTLFQNFQVAFHNVMTVATPRGKKEGFHHHNLISIMKVLIDALDLFCSTYTPRL 397
DB 358 ILFLIHLYLTNAFQALFAFVWSTYEFTLKCNFHNKKTEDIAIRIMAGVLQVLCSTYTPRL 417
OY 398 YALVTOMGSMKRSIFDEQTAALTLNMRNTAKERKKVYKVDIMLAOMIGDAPTSKGTSPM 457
DB 418 YALVTOMGSMKRSIFDEQTAALTLNMRNTAKERKKVYKVDIMLAOMIGDAPTSKGTSPM 469
OY 458 PSRASSPVHLHLHGMKRSDDP---SAPTSPTRMERAROMYPUVAHVHNLNADRRR 513
DB 470 PTHGMSPVHLHLHYNKRSIDQTSPTASPSRPSDYSGGH---GHQ-HFFDEDSQNH 524
OY 514 SVSSSALDAI-----PSADES 530
DB 525 STQREITDSFSSNHHPOVDMA 546

RESULT 6
H96640
Hypochemical protein p25B24.9 [imported] - Arabidopsis thaliana
C:Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 15-Jun-2001
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Accession: H96640
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lures, J.S.; Maiti, R.; Marzilli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96640
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-583 <STO>
A:Cross-references: GB:AE005173; NID:g4585879; PIDN:AA02552.1; GSPDB:GN00141
C:Genetics:
A:Gene: 125924.9
A:Map position: 1
C:Superfamily: barley pathogen resistance protein MLO

Query Match 44.6%; Score 1241; DB 2; Length 583;
Best Local Similarity 47.6%; Pred. No. 3.9e-100;
Matches 247; Conservative 86; Mismatches 138; Indels 48; Gaps 6;

QY 11 RTLPETPSMAVALFPAWVIYVSLLEHALHKLGHMFHKRKNALAELEKIKALMLVGF 70
DB 8 KLTLESTWAAVAVCFVLLLSIVLEIKLIGSWFKKRNKALYALEKVKALMLMGF 67
QY 71 ISLLAVTODPISGICISERKASIMRPS----- 99
DB 68 ISLLTIGGYTINICIPKNNLAASMPSCASEARRKYGKDDPKDEEENLRKLLQVLD 127
QY 100 --LPPSVSKYKXOYCAKKGKVSLSGSLHOLHIFVLAAPHVYSVIMALSRLM 157
DB 128 SLTPRSRLATKGYD-KCEKGVAVSAYGMHOLHIFVLAACHVLCYVYALKTGM 186
QY 158 RTWKWETASLEAYOPARPRFTHOTSPFKRHLSLSTPGIR-WVYAFRQFFRSV 216
DB 187 RHWKKEETKTEIEYXSHDEPRFRADTSFGRRLTFMSKSTLTIMVCFPRQFRSV 246
QY 217 TKVDYLLRAGFINAHLSHNS--KDFHKYIKRSMEDDFKVVGISLPLMCVALLFLFD 274
DB 247 TKVDYLLRAGFINAHLSHNS--KDFHKYIKRSMEDDFKVVGISLPLMCVALLFLFD 306
QY 275 IDGIGTLWISFIPVLVILCVGTEKLEIMALEIODRASYIKAPVPEPNSKFFMR 334
DB 307 TNGINSYMLPEIPVILVYGTGLQVITKGLRIQKRGDVVGFPLVOPGDHFFWEGR 366
QY 335 PDVVLFEIHLTFONAROMAFWVATVPLKCFHMHIGLSIMKVVYGLALDGLSYT 394
DB 367 PRIFLHLVLFNAQOLAFWVSTYEGKNCFHESRVYIIRISIGLVQILCSYV 426
QY 395 FPLVALVTOMGSKMRSTFDEQTKALTMKRNPAKEKKVNDTDLMAQMGATPSRGT 454
DB 427 LPLVALVTOMGSKMRPTVFNERVATLAKSHHTAKNNIKHGTS-----ESTPFSSR 479
QY 455 SPMPRASSPVHL-----HKMGSDDPQASPTSPKTE 489
DB 480 PTTPHGGSSPHLLNMRKRSRVSDESFANSSPRNED 518

RESULT 7
B84748
similar to MLO proteins from H. vulgare [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C:Accession: B84748
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617137
A:Accession: B84748
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <STO>
A:Cross-references: GB:AE002093; NID:g6598814; PIDN:AC69142.2; GSPDB:GN00139
C:Genetics:
A:Gene: ATG233670
A:Map position: 2
C:Superfamily: barley pathogen resistance protein MLO

Query Match 40.2%; Score 1119; DB 2; Length 501;
Best Local Similarity 47.3%; Pred. No. 1.4e-89;
Matches 237; Conservative 77; Mismatches 135; Indels 52; Gaps 10;

QY 11 RTLPETPSMAVALFPAWVIYVSLLEHALHKLGHMFHKRKNALAELEKIKALMLVGF 70
DB 15 RELDQPTWNAVSVGCVIILISIVLEIMHKIGSVTFERRKKALYALQIKNLMLVGF 74
QY 71 ISLLAVTODPISGICISERK--AASIMRPSLPPG-SYASKYKDY-----YC 114
DB 75 ISLLTFGQNYIASLCLVASRYGHAMSGPYDPSGSKKPKTTEHLERVLADAPQC 134
QY 115 AKKGVSIMSTGSLHOLHIFIFVLAAPHVYSVIMALSRLMRTWKWETASLEAY 174
DB 135 -KKGVPRLISNLHGVHIFEFVLAAPHVYSATIMVLRGAKIRGKWKVEEYVNI-DHEM 192
QY 175 ANDPARRFTHOTSPFKRHLSLSTPGIR-----WVYAFRQFFRSVYKVVYLLRAGT 229
DB 193 MNDPSRRLHETSFVREHV---NPMKKNFSFYVCFRQSLSVKRSIDLTKRIGFI 248
QY 230 NAHSHSKDFPKHYIKRSMEDDFKVVGISLPLMCVALLFLFDIGTLTWISFPL 289
DB 249 SVHLAPMKRNFQYIKRSLLEDDFKVVGISPELMAFVMLFLFDVHGMYATVITMIP 308
QY 290 VILCVGTEKLEIMALEIODRASYIKAPVPEPNSKFFMRPDVLFEGILLTFON 349
DB 309 LTLTATLQALISMALEIODRHAVALOGRLVNSDRHFWSRBALVLIHIFILFON 368
QY 350 AFQMANFVWVATVPLKCFHMHIGLSIMKVVYGLALDGLSYTFFPLVALVTOMGSKM 409
DB 369 AFETTYFWMVYFEGFGRSCFHHNFALLIIRVALGVGOFGLCSYITLPLVALVTOMGSTMK 428
QY 410 RSTFDEQTKALTMKRNPAKEKKVNDTDLMAQMGATPSRSPMS-----R 460
DB 429 RSVFDDQTSKALNMHKNKAKKSE-----TPGOTQPPRLNLRPKTGGDIE 473
QY 461 AASPVHLNR-GMGRSDPOS 480
DB 474 SASPANTASVDVKESDQOS 494

RESULT 8
F84552
similar to MLO proteins from H. vulgare [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C:Accession: F84552
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617137
A:Accession: F84552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <STO>
A:Cross-references: GB:AE002093; NID:g4914369; PIDN:AA032905.1; GSPDB:GN00139
C:Genetics:
A:Gene: ATG217480
A:Map position: 2

C;Superfamily: barley pathogen resistance protein Mlo

Query Match	Score	DB 2	Length
39.78	1106	574	

Matches	247;	Conservative	79;	Mismatches	161;	Indels	88;	Gaps	10;
---------	------	--------------	-----	------------	------	--------	-----	------	-----

2 AEDYEPARTLPETPSWAVALVEAVMIIVSVLLEHALHKLIGHWEHKKRKNALAELEKI 61

Oy 2 ADEYKRPARTLPSPMAVAVFAMVAVIYVULLEHAKHGHEHFKRKNALAELEKI 61
 Db 30 ADEKPKVYHAKQINQPIWAAVAACTFFIYVSLERKLHAKGVLMDBRKHTALLDALEKI 89
 Oy 62 KAEMLVGFISLLAVTQDPISGICISEKAASIMRCSLP----- 101
 Db 90 KAEMLVGFISLLTFGGQTYLLDICIPISVHARTMLPCPAPNLKREDDNGESHRLLSFE 149
 Oy 102 ----PSVSKRKDYCAKKGKAVIMSTGSLQHIFEFVLAVPHVYVIMALSRKM 157
 Db 150 HRFSLSGEASPIK---CTKREYVELLSAELMQHLLIFLATIRHYLSFTLMLGRLLKI 206
 Oy 158 RTMKKMETASLEQFANDPARPFTHOTSTYKNNLGL-STPGIRWVAVFPKPFERSV 216
 Db 207 RGMKHEMNTSSHNTEFSTDSRRLTHETISFRAHTSEFWTRIFEEFYVGCEFFRPFRSV 266
 Oy 217 TKVDYLLRAGEINAHLSHNSKEDFPHKYLTKRSMEDFEVWVGISLPLMCALLTFLEID 276
 Db 267 GRDYDYLLENGEIVAHNLAPGSGEFQKYLTKRLEDFKVVYGVSPVLMGSEFVELLMID 326
 Oy 277 GISTLWISFIPLYVLLCGKLEIMEMALIEDRASVYKSGAPVEESNPFMFHPHD 336
 Db 327 -----GKLDQAIMTRMALGITDRIAVAVQSGPVLQGNDEYFNGRPH 367
 Oy 337 WVFLEHLLLPQNAFQNAHPVYVATPGLKCKPFHNGISLTMKVYGLALQFLCSYTFEP 396
 Db 368 LILHLHMLPFLFNAQOLYTFPFWMYVSGSDSCYHNFENFIALVKYKALGVLGLCSYITLP 427
 Oy 397 LVALVTOMGSMNKRISIDEQTAKALTNMNRNTKEKKKRYDIDMLQMGIGADTPRGCTSP 456
 Db 428 LVALVTOMGSMRKKSVDEQOTSALKMKRMAVKKKKGVKATTRKLG---GDGSASTAST 484
 Oy 457 MPFRAS-----SPVHLHKGMSRDDPSA-----PISPRIMEARNDMP 496
 Db 485 VRSTSSVRSLQRYKTRPHSMRYEGL-----DEPSTLDIDNEALTPKSPSPFE----- 533
 Oy 497 VVYVAHPVHRLNPDARRRSVSSSALADIPSDPSF 531
 Db 534 LVVKYEPNKTNGETSR-----DTETDSKEFSF 561

RESULT 9
 B84552
 similar to M10 proteins from H. vulgare [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 15-Jun-2001
 C:Accession: B84552
 R:Lin, X.Y., Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 W.; Koo, H.; Molnar, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 Guss, D.; Niernm, W.C.; White, O.; Elsen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-766, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: AB4420; MIMD:20083487; PIMD:10617197
 A:Accession: B84552
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-580 <STO>
 A:Cross-references: GB:AE002093; NID:96598336; PIDN:AA86520.2; GSPDB:GN00139
 C:Genetics:
 A:Gene: AT2g17430
 A:Map position: 2
 A:Superfamily: barley pathogen resistance protein M10

[illegible]

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07 71 ISLLAAVQDEISGICISKK---AASIMRCSLPEGSVSKYK----- 110
      |||| | : : : ||| : : : |
Db 74 ISLLTFQNTIASICVPSRIGHAMSCFGPYDGPSEDDRKALKTTHAMRIIYSVRRSL 133
      |||| | : : : ||| : : : |
07 111 -----DYCAKKGKVSAMSTGSLQQLIEFTVLAAFHVYTSVIAALSLKLRPTWKMET 165

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Qy	166	EPASLEIYOFANDPARPRTFHOTSTYKKNL-GLSSTPIGRWYAFNQFRSTYKYDYL	224
Db	187	EXYIH-EQDMNDSRRRLHETISFVRHNVASMKFFEFYMCFFQDILRSYKSDYLW	245
Qy	225	RAGFTNAHLSHNSKRFPHKXIKIKRSMEDDFKVYVGSILPMLCVAILTFLDIDIGTLLWT	284
Db	246	RIGFTSYHLAPGKRFPOKXIKRSLIEDDFKVYVGSIRPELMAFWMLFLFLDYGVGWYAVI	305
Qy	285	SFPIVYLICVGRKLMIMEMALIEDODRASVYKAPRVBESKPMFMRPWWLEFTHL	344
Db	306	THIRPLETLAIGTKLQALISVMALEIGERRAVIQMPRVVNSDQHMEKPDVLVNIHF	365
Qy	345	TLFQNAFQMAHFUYATPAGTKKCFRNHITSLMUVGLDLOFSLSYTPRYALYOM	404
Db	366	VLFOEF-----GLMSCRHHNELLIRKVLGVGVFSLSYTPRLAYLYOM	413
Qy	405	GSNMKRSJEDQAKALTNWRTAKERKK	433
Db	414	GSTMKRSVFDQTSKALDEOMHNKARKTNE	442

RESULT 11

100621
 MIO vulgaris MIO protein homolog At2g44110 [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein F6E13.24
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 01-Feb-1999 #sequence__revision 01-Feb-1999 #text_change 15-Jun-2001
 C:Accession: T00691 #E84874
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, R.
 Submitted to the EMBL Data Library, June 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
 A:Reference number: Z14180
 A:Accession: T00691
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-496 <ROD>
 A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212880
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nleman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MWID:20083487; PMID:10617197
 A:Accession: E84874
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-496 <STO>
 A:Cross-references: GB:AEO02093; NID:g212880; PIDN:AAC23431.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: F6E13.24; At2g44110
 A:Map position: 2
 A:Insertions: 39/3; 59/1; 132/3; 171/3; 193/3; 222/3; 247/3; 277/2; 294/1; 307/3; 377/3; 407/3

```

0Y 171 EYOFANDPARRPETH--QISEPK-RHIGL-SSTPGIRWVAFFPQOFBSYTKVUULRLA 226
Db 184 EKXPTDQSIKRFHNOHEEFRSFGLVGRKADASGVOSFMOFLASVNSDITMRL 243
0Y 227 GFYNALHSHNSKEDFEHKYIKRSMEDDDKRVVVGISLPLWCAIILTFPIDIGLITWISF 286
Db 244 GFYTHCKTNKRFENFKYLMRALNSDDKRVVGSIMWLWVFWLLELNLINVAHWYFWMLAF 303
0Y 287 IPYVILLGVGKLEIMIMMALEIODASVYIKAPRVESKRFPMFHRDMLWFEFHLTL 346
Db 304 IPILILLVGVKLEHITITDLAEVAKEHINVEDDLVPRSDLPFWQSRRLVLEHIFIL 363
0Y 347 FONAFOAHFWYVATPRGLKCFEHNHIGLSIMKVVULGLAOLFOSITTEPRYALATWOGS 406
Db 364 FONSFEIAYFFFILOFGMDSCIDMHWKFIPLRYLGVAILDLSCTSPRLVALATWOGS 423
0Y 407 NMRSRPEOFOAKALNWNRTNTEKREKKVYRPTDMLAOMIGDATPSKQSPMPSRASPVH 466
Db 424 SEFGALFPMQJQHELWGMKMAKKRQVKKATQV-----GTSHDATSPRSIDLN-S 473
0Y 467 LHKHGKRSDDPOGAPPSRPTMEKRNDRVYVVAH 501
Db 474 LHKGSOONQ-----NPKRSE-----IAH 494

```

RESULT 12

hypothetical protein T10P11.12 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 15-Jun-2001
C:Accession: T01089
R:Kaplan, N.; Johnson, D.; Schutz, K.; Gnocj, L.; Hoffman, J.; Tili, S.; de la Bastide
hi, M.; Marienissen, R.; Chen, E.Y.; Wilson, R.; McComb, W.R.
submitted to the EMBL Data Library, November 1998
A:Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
A:Reference number: 214248
A:Accession: T01089
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1526 <RAP>
A:Cross-references: EMBL:AC003330; NID:g2622135; PTD:g3892049
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Intons: 61/1; 145/3; 184/3; 205/1; 237/3; 263/3; 309/1; 322/3; 392/3; 415/2; 435/3
A:Note: T10P11.12
C:Superfamily: barley pathogen resistance protein MLo

[illegible]

273 LDIDIGITLWISFIPVYLICVGTKEIMIMEMALEIODRASVIRKAPVPEPSNKKFFME 332
Db LNVGMHTYFMIAFIIPFALLAVGCKLEHVIQAQAEHVAEKVALLIEGDLVYKPSDEHFWF 364
333 HRPDWVLFIFHLTLFQNAFQNAHFWVAVATPGCKCFHHHIGLSTMKVYLGLAQFLCSY 392
Db SKQIVLYLHIFLFLQNAFELIAFFFWIWTYGFDSIMQVRYIYPRVIVGFIQVLCSTY 424
393 ITPFLYALVTOMGSNMKRSIFDEQTAALTNMNTAKKKKVTOTDMLMAQIMIGDATPSR 452
Db STPLVYAIYSQMGSSFKKAFEEENVQVIGVMAQYKKQR-----DLRAASNDDESSQ 479
453 -GTSPPMSRASSP 464
Db 480 AGPDPSSGSGAP 492

RESULT 13

T09888

hypothetical protein T22A6_80 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Jun-2001

C:Accession: T09888

R:Bevan, M.; Zimmermann, W.; Gruenleisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May

submitted to the Protein Sequence Database, June 1999

A:Reference number: 216896

A:Accession: T09888

A:Molecule type: DNA

A:Residues: 1-429 <BEV>

A:Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6_80

A:Experimental source: cultivar Columbia; BAC clone T22A6

C:Genetics:

A:Gene: ATSP:T22A6_80

A:Map position: 4

A:Insertions: 40/3; 60/1; 87/3; 126/3; 151/3; 177/3; 202/3; 232/2; 262/3; 331/3; 354/2; 374

C:Superfamily: barley pathogen resistance protein M10

Query Match

Best local Similarity 30.9%; Score 860.5; DB 2; Length 429;

Matches 180; Conservative 70; Mismatches 151; Indels 33; Gaps 5;

12 TLEPSPMAVALVFAVMITVSVLEHALHKLGHMFHKKRNALAELEKIKAEIMLVGFI 71
Db 8 SLEVTYVAVAFICFIYVLSLAEHGLHKLGRQODLFEALQKLEMLLGI 67
72 SLLAVTODPISGICISKASIMRPSCLPQSVSKYKDYCIYCAKKGVSIMSTGSLHQL 131
Db 68 SLMVLSQALRHICV-----PPA-----LGVPLVSYEALHQL 101
132 HIFFLAVFHTVYSVITMALSRLKMTKMKMETETASLETOFANDPARFETHTQTSFVR 191
Db 102 HIFFLAVFHTVYSVITMALSRLKMTKMKMETETASLETOFANDPARFETHTQTSFVR 191
192 RHLG--LSSTPGIRWVAFEPFOPFRSAYTKDYTLTLAGINAHLSHNSKDFPKYIKRSK 249
Db 162 MHAGGFWRSVYISWNSFFQFQSGVTSKSEYALQOAIMSHCHTNSDFPKYIMRL 221
250 EDDFKVVGISLPLWCVAIILFLDIDIGITLWISFIPVYLICVGTKEIMIMEMALE 309
Db 222 EIDFKKVVSIWYLMLEFVVYFLTNVGMNTYFMLSPLILLVAGKLEYIISLALD 281
310 IODRASVIRKAPVPEPSNKKFFWHRPDWVLFIFHLTLFQNAFQNAHFWVAVATPGCKCF 369
Db 282 VSEKSRRAEEA-VITPSEDLFWHRFGIYVQLHFLTLFQNAFELIAFFFWILFTYGHSC 340
370 HHHIGLSTMKVYLGLAQFLCSYITPFLYALVTOMGSNMKRSIFDEQTAALTNW----R 425
Db 341 MERIGTILIPRLVAGVYQVLCSTYSLPLVYALVTOMGSFKKGIQVNVQSTLEGWLEDR 400
426 NTAKEKKKVRDTM 439
Db 401 NNGESTSEAHREM 414

RESULT 14

T47469

hypothetical protein F18N11.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Jun-2001

C:Accession: T47469

R:Jordan, N.; Bangerl, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemc

submitted to the Protein Sequence Database, February 2000

A:Reference number: 224467

A:Accession: T47469

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-485 <JOR>

A:Cross-references: EMBL:AL132953

A:Experimental source: cultivar Columbia; BAC clone F18N11

C:Genetics:

A:Map position: 3

A:Insertions: 50/3; 70/1; 137/3; 176/3; 205/2; 225/3; 255/2; 272/1; 285/3; 343/3; 355,

A:Note: F18N11.50

C:Superfamily: barley pathogen resistance protein M10

Query Match

Best local Similarity 39.3%; Score 838.5; DB 2; Length 485;

Matches 188; Conservative 82; Mismatches 161; Indels 47; Gaps 7;

6 EYPPARTLPETPSMAVALVFAVMITVSVLEHALHKLGHMFHKKRNALAELEKIKAEI 65
Db 12 EVGAVRSIQETPMTALVTCFFIAVSLICELTILNLSTRKKRSTSLAEVEXLSYL 71
66 MLVGFISLLAVTODPISGICISKASIMRPSCLPQSVSKYKDYCIYCAKKGVSIMSTGSLHQL 111
Db 72 NVLGFMSMLAVTODPISGICISKASIMRPSCLPQSVSKYKDYCIYCAKKGVSIMSTGSLHQL 131
112 YTCACKGVVSLMSTGSLHQLHTIFPLAVFHTVYSVITMALSRLKMTKMKMETETASLE 171
Db 132 HCCSSKGTSLISEGLTQSLSTFFVLCMHLNCLNLLGMAKFFVYIHIDE--KME 189
172 YOFANDPARFETHTQTSFVRHILGLSTPGIRWVAFEPFOPFRSAYTKDYTLTLAGETNA 231
Db 190 FYGERDP-----NSGVSSK-----RQFVMSVAKVDYTLRLRGFI 226
232 HSHNSKDFPKYIKRSKDEDDPRVYVVGISLPLWCVAIILFLDIDIGITLWISFIPVYL 291
Db 227 HVSNNNAFNFQNTYQRLSHDEFTYVAGISPLMLTGVYIFMLDYSGMRVYFVMSVPLII 286
292 ILICVGTKEIMIMEMALEIODRASVIRKAPVPEPSNKKFFWHRPDWVLFIFHLTLFQNAF 351
Db 287 VLVICTKLEIMVAKMAVITIKENNSVIRGPIVESNDHFNPSNPRLLSLIHTLFTLTF 346
352 OMARFWVAVATPGCKCFHHHIGLSTMK---VVLGLAQFLCSYITPFLYALVTOMGSNM 408
Db 347 EMARFWVAVATPGCKCFHHHIGLSTMK---VVLGLAQFLCSYITPFLYALVTOMGSNM 406
409 KRSIFDEQTAALTNMNTAKKKK---VRDMLMAQIMIGDATPSRGTSPMSRASS 463
Db 407 KRAILEDQANVLEHMQVARDKKTIOPTDNNNNNGDI--DSGSSPVQTEVAS 462

RESULT 15

H86393

protein T24P13.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001

C:Accession: H86393

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al-

assen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kik

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Luo, Z.A.; Luo, J.S.; Maiti, R.; Marz

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal

ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: H86393

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-507 <STO>

A:Cross-references: GB:AE005172; NID:g9295722; PIDN:AAF87028.1; GSPDB:GN00141

C:Genetics:

A:Gene: T2AP13.8

A:Map position: 1

C:Superfamily: barley pathogen resistance protein M10

Query Match 23.0%; Score 641.5; DB 2; Length 507;

Best Local Similarity 31.8%; Pred. No. 7, 1e-48;

Matches 155; Conservative 72; Mismatches 131; Indels 129; Gaps 12;

```
QY 1 MAEDVEYPPARTLPETPPSMVAVLVFAVMIVSYLLEHALKLGHWFKRKNALAELEK 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MREETE-PSEKTLGLTPYMSVATVLTIFYVSLYERSIHLNMLQTKRKLPAALEK 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 IKAELMLVGFISLLAVTODPISGICISEKAAS-IMRPCSLPGSVKSKYKDYCAKK-- 117
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 MKEELMLGFISLLTATSTIANICVSSSFHNDREVPCT--PSEINEEESTISTVKRT 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 -----GKSLMSTGSLHQLHFFIFVLAVFHVTVYITMAL 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 QLTRSLFLHTLRRLKSGIGEDTCSGHEPEFLSYEGMDLHRFIFIMAVTHVYISCLTMLL 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 153 SRLKMRTWKKWETETASLEYQFANDPAREFTHOTSPVKRHLGLSTPGIRWVAFFROF 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 AIVKIHWRRIWEDE-----ICFFROF 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 213 FRSVTKVDYTLFRAGFIN-AHLSHN-SKPDFHKYIK-----RSM 249
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 199 GHSVVRSDYTLRKGFIMFANLFTLFRFFYLHSFAFIFVHLSIKKRMSTIYMISM 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 250 EDDKRVVVGISLPLMCVAIITFLDIDIGITLTWISFIPVILLCVGTLEMITMEALE 309
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 EEEFOKIVG-----RW-----LVLLVGAKLQHVIAITALE 289
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 310 ---IODRASVIKGPVVEPSNKFHFMRPDWVLFPIHLTLFONAFQMAHFVWTATPGIK 366
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 290 NASITEVYASGK---LRPDLELFWFKKPELLSLIHFIQONAFELASPFWPMWQFGYN 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 367 KCFHMHIGLSIMKVVGLALQFLCSTITPPLAALVTOGMSNMKRSIFDEGTAKALTNRN 426
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 346 SCFLRNHLVYLRLLIGFSQFLCSTYLPYALVTOGMYKAALLPORVRETINGMK 405
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 427 TAKEKKK 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 406 ATRRRRR 412
```

Search completed: November 18, 2002, 15:39:38
Job time : 45 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 14:37:47 ; Search time 25 seconds

(without alignments)
885.934 Million cell updates/sec

Title: US-09-857-896a-32

Perfect score: 2784
Sequence: 1 MAEDYEYPPARTLPETPSMA.....VSSSALDADIPSADFSFSG 534

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2434	87.4	533	MLO_HORVU	P93766 hordeum vul
2	1960	70.4	544	MLO_HORVU	O49873 hordeum vul
3	1839.5	66.1	540	MLO_ORYSA	O49914 oryza sativ
4	1281.5	46.0	576	MLO2_ARATH	O80961 arabidopsis
5	1119	40.2	501	MLO5_ARATH	O22815 arabidopsis
6	1068	38.4	580	MLO1_ARATH	O22752 arabidopsis
7	1062	38.1	560	MLO2_ARATH	O22752 arabidopsis
8	955	34.3	496	MLO1_ARATH	O80580 arabidopsis
9	932.5	33.5	526	MLO1_ARATH	O49651 arabidopsis
10	496	17.8	447	MLO3_ARATH	O23693 arabidopsis
11	427	15.3	217	MLO1_ARATH	O23693 arabidopsis
12	117.5	4.2	970	MLO1_ARATH	O23693 arabidopsis
13	103.5	3.7	1275	MLO1_ARATH	O23693 arabidopsis
14	98	3.5	353	MLO1_ARATH	O23693 arabidopsis
15	98	3.5	574	MLO1_ARATH	O23693 arabidopsis
16	97	3.5	2326	MLO1_ARATH	O23693 arabidopsis
17	96.5	3.5	439	MLO1_ARATH	O23693 arabidopsis
18	94.5	3.4	475	MLO1_ARATH	O23693 arabidopsis
19	94.5	3.4	506	MLO1_ARATH	O23693 arabidopsis
20	94.5	3.4	508	MLO1_ARATH	O23693 arabidopsis
21	94.5	3.4	510	MLO1_ARATH	O23693 arabidopsis
22	93.5	3.4	595	MLO1_ARATH	O23693 arabidopsis
23	92	3.3	339	MLO1_ARATH	O23693 arabidopsis
24	91.5	3.3	355	MLO1_ARATH	O23693 arabidopsis
25	91	3.3	332	MLO1_ARATH	O23693 arabidopsis
26	90	3.3	333	MLO1_ARATH	O23693 arabidopsis
27	89.5	3.2	369	MLO1_ARATH	O23693 arabidopsis
28	89.5	3.2	568	MLO1_ARATH	O23693 arabidopsis
29	89	3.2	443	MLO1_ARATH	O23693 arabidopsis
30	89	3.2	1278	MLO1_ARATH	O23693 arabidopsis
31	88.5	3.2	607	MLO1_ARATH	O23693 arabidopsis
32	88	3.2	345	MLO1_ARATH	O23693 arabidopsis
33	87.5	3.1	355	MLO1_ARATH	O23693 arabidopsis

34	87.5	3.1	1008	1	DPOL_HSV2	P52367 equine herp
35	87.5	3.1	1786	1	YCPL_ARATH	P56785 arabidopsis
36	87.5	3.1	2051	1	FASL_YEAST	P07149 s fatty ac1
37	87	3.1	443	1	HELSD_HELPY	O25254 helicobacte
38	87	3.1	650	1	VEI_HPV73	O82007 human papil
39	87	3.1	669	1	OATR_RAT	P70502 rattus norv
40	87	3.1	875	1	TRAC_ECOLI	P18004 escherichia
41	86.5	3.1	875	1	LENI_BACST	O8185 bacillus st
42	86	3.1	338	1	YDA9_THENA	O91170 thermocoga
43	86	3.1	524	1	GTR2_HUMAN	P1168 homo sapien
44	85.5	3.1	439	1	NFIC_CHICK	P17926 gallus gall
45	85	3.1	348	1	EMLI_PONBY	P79236 pongo pygma

ALIGNMENTS

RESULT 1	MLO_HORVU	STANDARD;	PRT;	533 AA.
ID	MLO_HORVU			
AC	P93766;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	MLO protein.			
CN	MLO.			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxID=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.			
RC	STRAIN-Various strains; TRISUP-leaf;			
RX	MEDLINE=97207016; PubMed=9054509;			
RA	Bueschges R., Hollticher K., Panstruga R., Simons G., Wolter M.,			
RA	Rijters A., van Daelen R., van de Lee T., Diergaarde P.,			
RA	Groenendijk J., Toepesch S., Vos P., Salamini F., Schulze-Lefert P.;			
RT	"The barley Mlo gene: a novel control element of plant pathogen			
RT	resistance.";			
RL	Cell 88:695-705(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Ingrid;			
RX	MEDLINE=96128007; PubMed=9461468;			
RA	Panstruga R., Bueschges R., Piffanel P., Schulze-Lefert P.;			
RT	"A contiguous 60 kb genomic stretch from barley reveals molecular			
RT	evidence for gene islands in a monocot genome.";			
RL	Nucleic Acids Res. 26:1056-1062(1998).			
CC	- FUNCTION: MAY BE INVOLVED IN DOWN-REGULATING LEAF CELL DEATH AND			
CC	PATHOGEN DEFENSE FUNCTIONS.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	- MISCELLANEOUS: REF.1 HAS SEQUENCED MLO IN STRAINS CV. CARLSBERG			
CC	II, CV. DIAMANT, CV. FOMA, CV. HAISA, CV. INGRID, CV. MALTERIA			
CC	HEBA, AND CV. PLENA.			
CC	- SIMILARITY: BELONGS TO THE MLO FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; 283834; CAB06083.1; -			
DR	EMBL; Y14573; CAAT4909.1; -			
DR	InterPro; IPR004326; MLO.			
DR	Pfam; PF03094; MLO; 1.			
KW	Plant defense; Transmembrane; Pathogenesis-related protein.			
FT	TRANSMMEM 18 38			POTENTIAL.
FT	TRANSMMEM 63 83			POTENTIAL.
FT	TRANSMMEM 132 152			POTENTIAL.

ID	MLH1_ORYSA	STANDARD;	PRT;	540 AA.
AC	049914;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	MLO protein homolog 1.			
GN	OSMLO1 OR MLO-HL			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Eurhaptophyceae; Oryzeae; Oryza.			
OX	NCBI_TaxID=4530;			
RA	SEQUENCE FROM N.A.			
RC	STRAIN=CV. IR-B921;			
RA	Panstruga R.;			
RL	Submitted (May-2002) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (potential).			
CC	-1- SIMILARITY: BELONGS TO THE MLO FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; Z95353; CAB08606.2; -			
DR	InterPro; IPR004326; MLO.			
DR	Pfam; PF03094; MLO; 1.			
KW	Transmembrane.			
FT	TRANSMEM 17 37	POTENTIAL.		
FT	TRANSMEM 63 83	POTENTIAL.		
FT	TRANSMEM 143 163	POTENTIAL.		
FT	TRANSMEM 266 286	POTENTIAL.		
FT	TRANSMEM 288 308	POTENTIAL.		
FT	TRANSMEM 348 368	POTENTIAL.		
FT	TRANSMEM 384 404	POTENTIAL.		
FT	SEQUENCE 540 AA; 60707 MW; 7FE576B03A91ADBE CRC64;			
SO	SEQUENCE			
Query Match	66.1%;	Score 1839.5;	DB 1;	Length 540;
Best Local Similarity	67.7%;	Pred. No. 1.3e-143;		
Matches 366;	Conservative 59;	Mismatches 87;	Indels 29;	Gaps 9;
OY	10 ARTLPETSMANAVLVFVAMVIIVSVLEHNLKLGKHPKRRKRNKALAELEKIKAEMLVVG 69			
DB	8 SRELPEPTPMANAVVAVCAVLVLVAASAMEGHNLHLSHWPERRRQKAMGDALDKIKAEMLVG 67			
OY	70 FISLLIAVTAOPISGIGTISSEKASIMRCSLPSPGSVSKKD-----YYCAK-K 117			
DB	68 FISLLIVTAQAPISKICIPKSAANILLPKKAGQDIEELKASGRSLGAGAGGDSKFP 127			
OY	118 GKVSLMSTGSLHQLHIEFVLAVFHVTVSVIIIMLSIKMKRTKKKKEETASLEYORAND 177			
DB	128 GKVALVSAKSMHQLHIEFVLAVFHVTVCIITMGIGLKKKKKKKESQINSLEYORAPD 187			
OY	178 PAFEFRTHTQTSFVVRHLG-LSSPTGIRMYVAFFPPQPRSVTKVDYTLTRAGGINAHLSH 236			
DB	188 PSEFRTHTQTSFVVRHLGSSPTGIRMYVAFFPPQPRSVTKVDYTLTRAGGINAHLSH 247			
OY	237 SKKDFPKIKRSMEDDFKVVVVGISLPLMCVALITLFLDIDIGTLITWISFIPVLILCVG 296			
DB	248 SKKDFPKIKRSLDEDDKVVVVGISLPLMVGILVFLDIDIGTLITWISFVPLITIVLVG 307			
OY	297 TKLEMIIMEMALEIQDASVYKAPAVESSKKEFWRRPVMVLFETHILTRPOMFOAHF 356			
DB	308 TKLEMIIMEMAOEIQDASVYKAPAVESSKKEFWRRPVMVLFETHILTRPOMFOAHF 367			
OY	357 VVTVAPPGIAKCFPMHIGLSIMKVVVLGALQDSCSYTPPLVALVYQMSNKKRSTDEQ 416			
DB	368 VVTVAPPGIAKCFPMHIGLSIMKVVVLGALQDSCSYTPPLVALVYQMSNKKRSTDEQ 427			

```

OY 417 TAAALNNMNTAKKKKRCPTDMLNMQIGD-APPSSGTSIPMSRASSPVHLHKNGRS 475
DB 428 TAAALNNMKKAAMKKKKRYADAFLLQMSVDPATPA-----SSRASVHLLDDHRRS 481
OY 476 DDEQSAPT--SPRTMEARDMYPPVVVAHPVRLT--NPADRRSRSSSSALDAPSDASF 531
DB 482 DDPESTITVASPAPAE--DMYVPVPAASROLLDDPDPRMMWASS---ADIADPSFSF 536
OY 532 S 532
DB 537 S 537

RESULT 4
ML12_ARATH STANDARD; PRT; 576 AA.
AC 080961; Q94KB3;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE MLO-like protein 12 (AtMlo12).
GN MLO12 OR ATG39200 OR TICB24.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Devoto A., Hartmann H.A., Pfiffenell P., Elliott C., Simmons C.,
RA Taratuno G., Goh C., Cohen F.E., Schilze-Leferst P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the
RL plant-specific seven transmembrane MLO family." ;
RN Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RX Lin A., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffit K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Coppenhafer G.P., Preuss D.,
RA Nielsen W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C. ;
RN "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: BELONGS TO THE MLO FAMILY.
-----
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CC CC
DR EMBL; AF369573; AAK53805.1; -
DR EMBL; AC004697; AAC28997.2; -.
DR InterPro; IPR004326; MLo.
DR Pfam; PF03094; MLo.1.
KW Transmembrane; Multigene family.
FT TRANSMEM 14 34 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
FT TRANSMEM 279 299 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
FT TRANSMEM 363 383 POTENTIAL.
FT TRANSMEM 406 426 POTENTIAL.
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SEQUENCE 576 AA: 66548 MW: 43D9F6AED64DBE6 CRC64:

Query Match 46.0%; Score 1281.5; DB 1; Length 576;

Best Local Similarity 46.4%; Pred. No. 1e-97; Mismatches 261; Conservative 86; Mismatches 138; Indels 57; Gaps 10;

11 RTLPETPSMAVALVAVAMIVSVLLEHALHKGHWHRHKKALAELEKIKALMLVGF 70
12 RSEETPMVAVAVAVCFLLIFISIMIEYFLHFGHFKKHKKALSEALEKVMELDGF 65
66 ISLLAVLQTPVSEICIPRNIAATMPCS- NHQEIATYGGDIYDQKRLDEPDSNDFY 123
71 ISLLAVTQDPIGICISSEKASIMRCSLPGSVKSY-KDY- 113
114 -----CAKKVSLMSTGSLHQLHIFVLAVFHVTVYIIMALSRLKMTW 160
124 SPRNIAATKGYDKCAEKQALVSAVGIHQHIFVLAHVHVLCTITVALGKTMKKW 183
161 KKMEPTASLEFOPANDPARFRTHOTSPVKRHLGL-SSTPGIMVAVAFRPFPSVTKV 219
184 KSMERETITIEYOYANDPERFRADTSFRHNLIMSKSTFIMTICFPFROPFGSVTKV 243
220 DYTLRAGFINAHLSHNS--KDFHNYIKRSMEDFKVYVGLSLPWCVAIITLFLDIDG 277
244 DYTLRHGFIMAHLPAGSARFDFQYKIERLEODFTVVGISPLIMCIATVLEILNTHG 303
278 IGTLMWISFIFLVILLCVGTLMITIMEMALIODRASVIGAPVPSKPFMRPDM 337
304 KDSYLMLEFLLIYILVIGAKLQIMISKGLIOKGVAVGAVVPSGDLFWFRPRPF 363
338 VLPEHILTLFQNAFQMAHFWYVAVFGLKCFHMHIGLSIMKVVGLALDGLSYTFEPL 397
364 ILFLHLVLFNAQLAFVWSTYEFTLKNCFHMHIGLSIRITMGVLIDVLCSTYITLPL 423
398 VALVQMGSMNKRISIFDEQATKALTMKRTAKKKVADTQMLAQMIGDAPRSGTSPM 457
424 VALVQMGSMRPTIFNDRVANALKKMHTAKKOTKHH- -GNTPHSRPT 475
458 PSRASPVHLHKMGKSDPO- -SAPTSPTMEERKDMRYVAVHRYHNLNADRRR 513
476 PTHGMSPVHLHNYNRSIDQSTFTASPSRPFSDYSGQH- -GHQ-HFPDPSQNH 530
514 SVSSSALDADI- -PSADFS 530
531 SYOREITDSEFSNSHHPQVMA 552

RESULT 5
MLOS_ARATH STANDARD; PRT; 501 AA.
ID MLOS_ARATH
AC 02815;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE MLO-1ike protein 5 (AtMLO5).
GN MLOS OR AT2G33670 OR FAP9.44 OR T01B08.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA Taramino G., Goh C., Cohen F.E., Schulze-Lefer P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the
RT plant-specific seven transmembrane MLO family.";
RL submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cy. Columbia;
RX MEDLINE=20083487; Pubmed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Cready T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC -----
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CC -----
CC EMBL: A6369566; AAK53798.1; -
CC EMBL: AC002332; AAM14803.1; -
CC EMBL: U78721; AAC69142.3; -
CC InterPro: IPR004326; MLO.
CC Pfam: PF03094; MLO; 1.
KW Transmembrane; Multigene family.
FT TRANSMEM 23 POTENTIAL.
FT TRANSMEM 63 POTENTIAL.
FT TRANSMEM 152 POTENTIAL.
FT TRANSMEM 172 POTENTIAL.
FT TRANSMEM 274 POTENTIAL.
FT TRANSMEM 294 POTENTIAL.
FT TRANSMEM 296 POTENTIAL.
FT TRANSMEM 360 POTENTIAL.
FT TRANSMEM 380 POTENTIAL.
FT TRANSMEM 392 POTENTIAL.
FT TRANSMEM 458 POTENTIAL.
FT CONFLICT 458 MISSING (IN REF. 1).
SQ SEQUENCE 501 AA: 56896 MW: 4B3F95D0FB18D0CF8 CRC64:
40.2%; Score 1119; DB 1; Length 501;
Best Local Similarity 47.3%; Pred. No. 2e-84; Indels 52; Gaps 10;
Matches 237; Conservative 77; Mismatches 135; Indels 52; Gaps 10;
11 RTLPETPSMAVALVAVAMIVSVLLEHALHKGHWHRHKKALAELEKIKALMLVGF 70
15 RLDQPTMAVSTGCVIILISIVLEIMIKHIGEVFTERRKALYEAQIKENLWLVGF 74
71 ISLLAVTQDPIGICISSEK- -AASIMRCSLPG-SVSKSYKDY- -YC 114
75 ISLLTFGQNTYASLCAVSRGHAASFCGPDGSGSKKPKTTTLERRLADAPAC 134
115 AKKGVSLMSTGSLHQLHIFVLAVFHVTVYIIMALSRLKMTWKWETASLEYOF 174
135 -KKGYVPLISLANLQHVHIFFLAVFHVTVYIIMALSRLKMTWKWEEVEVIN-DHEK 192
175 ANDPARPRTHOTSPVKRHLGLSSIPGR- -WVAFRPFPSVTKVYLRLRGFI 229
193 MNDPSRFLRHETSPVREHV- -NPAKNRSEFYCFRQMLSVKSYLTKRGGFI 248
230 NAHLSHNSKDFEHYIKRSMEDDKVYVGLSLPWCVAIITLFLDIDGIGTLTWISFPL 269
249 SVHLAPMKRNFQYKIKSLDEDDKVVYVGLSPELMFVMLFLFVHGMYTAVITMIP 308
290 VILLCVGTLMITIMEMALIODRASVIGAPVPSKPFMRPDMVLEFHLTLFON 349
309 LTLTLAGTKLQALISOMALETOBRHVAVQGLPWNSDHNFSPRALVLIHIFLIFON 368
350 AFQMAHFWVAVTPGLKCFHMHIGLSIMKVVGLALDGLSYITFPLVALVTMGSMNK 409
369 AFETTYFWIWEFGIRSCFHHHFFALITIRVALGVGVOFLYITPLVALVTMGSTMK 428
410 RSTFDEQATKALTMKRTAKKKVRODTQMLAQMIGDAPRSGSPMPS- -R 460
429 RSVFDDQTSKALNMHKKKNS- -TPQOTOPPLNLRPKTGDDIE 473

OY 461 ASPVHLHK-GMGREDDPOS 480
 DB 474 SASPANTASVDYKESDOSQS 494

RESULT 6

YML2_ARATH
 ID YML2_ARATH STANDARD: PRT: 580 AA.
 AC 022752;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical MLO-like protein At2g17430.
 GN At2g17430 OR F5J6.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 CC eucosids II: Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.

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DR EMBL: AC002329; AAB86520.2; -
 DR InterPro: IPR004326; MLO; 1.
 DR Pfam: PF03094; MLO; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 62 82 POTENTIAL.
 FT TRANSMEM 196 216 POTENTIAL.
 FT TRANSMEM 258 278 POTENTIAL.
 FT TRANSMEM 319 339 POTENTIAL.
 FT TRANSMEM 346 366 POTENTIAL.
 FT TRANSMEM 445 465 POTENTIAL.
 SQ SEQUENCE 580 AA: 66723 MW: AEF812A531E7EDAF CRC64;

Query Match 38.4%; Score 1068; DB 1: Length 580;
 Best Local Similarity 46.9%; Pred. No. 37e-80;
 Matches 223; Conservative 67; Mismatches 131; Indels 54; Gaps 6;

OY 11 RTPEPSSNAVALFRAVMIYSLLEHALKLGH----- 44
 DB 31 KELSQTPTMAVAVVCTFFILSHLEKGLQRLANVCFLLLLLFLRVFLFKHSLETFEE 90
 OY 45 ----WFKRKKNALEALEKIAELMVGFSILLAVTODPISGICISEKASIMRPC-- 98
 DB 91 VSSQWLKKKKHNSLLEALEKIAELMIGFISILLTFEGEPIYLIKCVRKALMLPCLIS 150
 OY 99 -----SLPGSVKSKY-----KDIYCAKKGKYSLSMSTGSLHQLHITFVLAVFHTYS 146
 DB 151 EDTVLFOKLAPSSLSRHLNLAAGDTISINC-RQGESEPLITLKGHQLHLLFLFLAIFHTIYS 209

OY 147 VTIATSLRKMTKKMETETASLEFQFANDPARRFPHQTSFYKRLGL-SSTPGIRRV 205
 DB 210 LITMMLSRKIRGNKKRKEOETLSNDSEFISIDSRILRTHETSFVREHTSWTTPPFYV 269
 OY 206 VAFRFQFFSVKYVDLTLRAGFTINAHLSNKKPFDHFKYIKRSMEDDFKVVGISPLKC 265
 DB 270 GCFPFQFVSVERDYLTLRHGFTISHLNAPGKRFNFQYIKRSLDEDFKLVGISVYLA 329
 OY 266 VALLLFLDIDIGITLWISFIPVLVLLCVGKLEMTIMALEIQRASVIGAPVEP 325
 DB 330 SFVITFLNVGWMTLFWASIPPLITLIVGTRKQAIKATATALIVETHAVVQGMPLVYG 389
 OY 326 SNKFWFHRPDVWLFETHLFLFONAFOMAFWYATFGALKCFPHMIGSLIKVYGLA 385
 DB 390 SDRYFWPCDQLLHLHFLPQNAQOITHFWIMKYSGLKSCCHKPFLVSKLCLCG 449
 OY 386 LQFLCSYITFPYLAVT-----OMGSNMKRSIFDQYAKALTNMRTAKKK 432
 DB 450 ALILCSYITLPLVATVQMKNKCVQMGSHMKKAVFDBQMAKALKKWKDKIKLK 504

RESULT 7

YML2_ARATH
 ID YML2_ARATH STANDARD: PRT: 560 AA.
 AC 022757;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical MLO-like protein At2g17480.
 GN At2g17480 OR MJB20.4 OR F5J6.23.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 CC Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae:
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.

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 CC -----

DR EMBL: AC002329; AAB86524.1; -
 DR InterPro: IPR004326; MLO; 1.
 DR Pfam: PF03094; MLO; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 12 32 POTENTIAL.
 FT TRANSMEM 47 67 POTENTIAL.
 FT TRANSMEM 93 113 POTENTIAL.
 FT TRANSMEM 182 202 POTENTIAL.
 FT TRANSMEM 305 325 POTENTIAL.
 FT TRANSMEM 397 417 POTENTIAL.
 SQ SEQUENCE 560 AA: 63247 MW: EAAAG9CF15A6AF49 CRC64;

ID MLO1_ARATH STANDARD: PRT: 526 AA.
AC 049621; 022766;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MLO-like protein 1 (AtMLO1) (MLO protein homolog 1) (AtMLO-H1).
GN MLO1 OR MLO-H1 OR AT4G02600 OR T10P1.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Hamdout R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetalle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohenseil J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grynoprez B., Chung Y.-J., Vandenbusche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Ramsperger U., Hildert H., Braun M.,
RA Holter E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooljain P., Klein Lanckhorst R., Rose M., Hauf J., Koetter P.,
RA Bernleiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen A., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,
RA Pettett A., Ralndream M.A., Lyne M., Benes V., Rechmann S.,
RA Borova D., Bloecker H., Scharfe M., Grimm M., Lehnert T.-H.,
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RA Gabel C., Fuchs M., Farman B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argitlon A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muehlen A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedorf F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Jacou D., Jesse T.,
RA Heijnen L., Schwarz S., Scholier P., Heber S., Frances P., Bieleke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Farnell L., Dedila N., Gnoj L., Schult K., Huang E., Spliegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spleth J., Ryan E., Andrews S., Giesel K., Layman D.,
RA Du H., All J., Bergthoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekhar M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granat S., Shohdy N., Hasegawa A., Hamed A., Iodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McComble W.R.,
RT *Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana*;
RL Nature 402:769-777(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC -----
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CC -----
DR EMBL: 295352; CAB08605.1; -
DR EMBL: AC002330; AAC78258.1; ALT-SRQ.
DR EMBL: AL161494; CAB80753.1; -
DR InterPro: IPR004326; MLO.
DR Pfam: PF01094; MLO.1
KW Transmembrane; Multigene family.
FT TRANSMEM 12 32
FT TRANSMEM 62 82
FT TRANSMEM 161 181
FT TRANSMEM 288 308
FT TRANSMEM 309 329
FT TRANSMEM 373 393
FT TRANSMEM 413 433
SQ SEQUENCE 526 AA; 59126 MW; 8B63C276A71A9768 CRC64;
Query Match 33.5%; Score 932.5; DB 1; Length 526;
Best Local Similarity 40.2%; Pred. No. 4,5e-69;
Matches 198; Conservative 79; Mismatches 167; Indels 49; Gaps 8;
QY 12 TLPEPSAVAVLFAVAVIIVSVLLEHALHKIGHFHKRKNMALAELEKIKELMLVGF 71
DB 9 SLEETPLVAVAGVCTVVAISLAVBERLLHFGYLVKKRKOKPLYLEALQKKEELMLLGF 68
QY 72 SLLAVYQDPLSGICISKEASIMRCSLPG-----SVSKYKDY----- 112
DB 69 SLLVTVQGLSKFKCVKENVLMHMLPCSLDSRBAGASEHKVNTAKEHQFLVYGTR 128
QY 113 -----CAKKGVSLSGSGSIHOLHIFFLAVAEHTVSVIIMLSRKMKTW 160
DB 129 RLLEHNAVYQCSSEKGVPLISEALHHHLHITFLVLAISVTFCLVIVFGSTRHQM 188
QY 161 KKEETEPASLEVFANDP-----AREFTHQTSFVRR-LGLSTPGI-RWVVAFFPFO 212
DB 189 KKWEDSIADK-----DPTALRRKRRVYVNHNAFIEHFLGIGKDSVILGTSFLKQF 244
QY 213 FRSYTKVDYTLTRAGFINHLSHNSKPFHXYIKRSDEDFKVVGSILPLMCVALILTF 272
DB 245 YDSYTKSDYVTLTAGSIMHNCGNKMLFKHYMRALAEDEFKQVGSITWLMIFVILL 304
QY 273 LDIGIGITLWISFIFLVLLCGVKLEMIIMEALEIDORASVTKGAPVEPSKKEFWF 332
DB 305 LNVGMHTYFWIAFIFFALLAVGKLEHVAIQLAHVAEKAHVAEGDVLVYPSDEHFWF 364
QY 333 HRPDVLFFHILTFQNAFQMAHFVWVATPGTKCPFHMHIGLSIKKVVILGALQPLCSY 392
DB 365 SKPQIVLYLHFLFQNAFEIAFFWIMVWTYGFDSCLMGVRYIVRLVIGVFTDLCSTY 424
QY 393 ITFFLVAVYQGSNNKRSIFDEQTAKALVWNTAKKKKRYBDMLMAQIDATPSR 452
DB 425 STPLVAVISQMSKSKRAIFENYQVLGMAQVKYOKR-----DLKAAASNDGESSQ 479
QY 453 -GTSMPSPRASSP 464
DB 480 AGPPDGSAGAP 492
RESULT 10
YML3_ARATH
AC 023693;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical MLO-like protein Atlg11000.
GN Atg11000 OR T19D6.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

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OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv, Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altsch H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizat L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luores J.S., Maiti R., Marzilli A.,
RA Miltcher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaja V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.";
RL Nature 408:816-820(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U95973; AAB5495.1; -
DR InterPro: IPR004326; MLO.
DR Pfam: PF03094; MLO; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 14 34 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 247 267 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
SQ SEQUENCE 447 AA; 50608 MW; 027A1C33AE1B5EEA CRC64;

Query Match 17.8%; Score 496; DB 1; Length 447;
Best Local Similarity 26.0%; Pred. No. 2.8e-33;
Matches 133; Conservative 76; Mismatches 156; Indels 146; Gaps 12;

OY 11 RPLPTPSMAALVFAVMITIVSYLLEHLLKLG--HMFHRRHKNALAELEKIKELMLV 68
DB 9 RSLAETPTYSASVTVLVFVCELVERRAIVRPGKDYGIHKK----- 49
OY 69 GFISLLAVTODPIISGICSEKASIMRPSLPGSVSKYKDYCAKKGKSLMSTGSL 128
DB 50 ----VLEHT-----SSTNOSLPHNGIHE--ASHOCG-IGRPFPYSGL 88
OY 129 HOLHFFIVLAVFHYTVSYVIALSLKMKRWKKEFETASLEQVANDPAPFRTHQS 188
DB 89 EQLRLFLVGLTHVLVSGTALGASKL----- 117
OY 189 FVKRHGLSSTPGIRWVVAFFROFERSVTKVDYTLRAGFINAHLSHNSKF--DFHKYIK 246
DB 118 -----CPLRFGSIRKSDYFALRIQGLT---KHNLPTFYNFHMVAV 156
OY 247 RSMEDDFKVVVGLSLPWCVAITLFLDIDGIGTILTSFPLVILLYCGTKEMINEM 306
DB 157 RIMEDEFHGIAGISWPLMVAIVICINHGGLNMTFWLSFPALILVGTIKLHNVSKL 216
OY 307 ALEIODRASVITKGAPEVPSNKFPMFHRDPDWL-----FFIHLTLFONAFOMAHF 356

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DB 217 ALEVEKOOTGTNSGAQVKAPEADGLFMEGKEPILLRLIOFIIFOMILLYFLIMONAEEMATF 276
OY 357 VWTVAITPCLKPKCFMHMIGLSIMKVVGIALOFLCSYIEFPFLYALVYOMSGNMKRSIPBEQ 416
DB 277 IMFV-----FWCYGIVPLNLYVYOMSGRHKKAVNES 309
OY 417 TAKALTNMRNTRAKKK-----VRDTMLQMAQMGDTSPSGTSPMPSRASSP 464
DB 310 VQDSLSHMCVKRKRKSTRVCSLDTATIDRDEDMVGTLSRSSWTSILNQITNSIDQ 369
OY 465 VHLHKGGRDDPSQASPTSPRTMERADMY 495
DB 370 AHSIFGAASSSPDDGYTS-RVEEYLSETY 399

RESULT 11
MLOL.LINUS
ID MLOL.LINUS STANDARD; PRT; 217 AA.
AC P81785;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MLO-like protein (Fragment).
OS Linum usitatissimum (Flax) (Linseed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Linaceae; Linum.
OX NCBI_TaxID=4006;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv, Antares; TISSUE=Ovary;
RA McKay G.J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC -----
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CC -----
DR EMBL: AJ005341; CAA06487.1; -
DR InterPro: IPR004326; MLO.
DR Pfam: PF03094; MLO; 1.
KW Transmembrane.
FT NON_TER 1 1
FT TRANSMEM 35 55 POTENTIAL.
FT TRANSMEM 59 79 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT NON_TER 217 217
SQ SEQUENCE 217 AA; 24604 MW; 4341CE37FC2EB493 CRC64;

Query Match 15.3%; Score 427; DB 1; Length 217;
Best Local Similarity 56.1%; Pred. No. 5.3e-28;
Matches 83; Conservative 20; Mismatches 43; Indels 2; Gaps 1;

OY 225 RAGFINAHLS--HNSKDFHKKYIKRSMEDDFKVVGISLPLWCVAITLFLDIDGIGTIL 282
DB 5 RYFIILAHNLAPGESERDFQKYVNRSLDEDFKVVGISLPLWFVLELLSNHGWAVL 64
OY 283 WISFIPVLVLLCVGTRKLEMTIMEALFIDORASVITKGAPEVPSNKFPMFHRDPDWLFFL 342
DB 65 WLFPFILLIILVVGTRKLOVITTOGSLSDRGVNVKGAPEVPGDDLFWEGRPLVLELI 124
OY 343 HFLFONAFOMAHFWVATPGLKCFH 370
DB 125 HFLFONAFOLAFILMSYVEEGITCFH 152

RESULT 12

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Y277_MYCGE
ID Y277_MYCGE STANDARD: PRT: 970 AA.
AC 049409: 049253:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG277.
GN MG277.
OS Mycoplasma genitalium.
OC Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxId=2097;
RN [1]
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fleischman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lucier J.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 624-678 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bort K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J.Bacteriol. 175:7918-7930(1993).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC EMBL: 039707; AAC71499.1; -
DR EMBL: 002116; MAD12390.1; -
DR TIGR: MG277; -
KW Hypothetical protein; Transmembrane; Complete proteome.
KM
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 515 535 POTENTIAL.
FT TRANSMEM 537 557 POTENTIAL.
FT TRANSMEM 558 578 POTENTIAL.
FT TRANSMEM 614 634 POTENTIAL.
FT TRANSMEM 645 665 POTENTIAL.
FT TRANSMEM 726 746 POTENTIAL.
FT TRANSMEM 762 782 POTENTIAL.
FT TRANSMEM 789 809 POTENTIAL.
FT TRANSMEM 816 836 POTENTIAL.
FT TRANSMEM 877 897 POTENTIAL.
FT TRANSMEM 903 923 POTENTIAL.
FT DOMAIN 50 53 POLY-THR.
FT DOMAIN 370 382 POLY-ASN.
FT CONFLICT 673 678 SGANMK -> OVOKKA (IN REF. 2).
SO SEQUENCE 970 AA; 108163 MW; F106CDECC9BD44FF CR664;

Query Match 4.2%; Score 117.5; DB 1; Length 970;
Best Local Similarity 18.9%; Pred. No. 0.097;
Matches 100; Conservative 92; Mismatches 177; Indels 161; Gaps 25;

QY 8 PPARLPETPSMAVALY-FAVMITIVSLLEHLKHLGHMFHRRKRNALALEKIKAEILM 66
DB 504 PLANTITDVSNFASFIAGFIIVLIAAVLLTRKYLGLY-----KALALGLSVSSLVI 558
QY 67 -----LVGFISLLAYTOPDISGICISF-----KAASIMRCSLPSSVASKTK 110
DB 559 FSANGVVDVFSFVGIFPVIAINLNLNLGELFLRNIRNNASTIESWKL----- 608

QY 111 DYVCAKKGKVSIMSTGSLHQLHIFVLAVFHYV---SVIIMALSRLKRTWKMETET 167
DB 609 ---CLKRS-----FEANLEFHIWLSALVVIYSNYQV----- 640
QY 168 ASLEKOPFNDDA-----RPERHTQTSFVRNRLGLSTGTGIMVVAFFROFBSVTVV--D 220
DB 641 -----QLANLMAISAITSYFSFGISIVLISLFSVSESGAMWKLFLYOKDAKALVTSSEN 695
QY 221 YTLTRAG-----FI--NNA--LSHNSKPDF-----HKYI 245
DB 696 YSLSTSDLTNDFFITRKNQHDFFLKNMKFLFVLLILAGVWLVLYLVQNLNGEFL 755
QY 246 KRSMEDDFKVVVAGISLPLMCVALTLLEFDIDISGLTWISPIPLVILLCGIKLEMIIE 305
DB 756 ADVVSSNGITAGIGT---VSLYLATYCLIRGAYGLSVLISFLLCSGLFPAVWVLTN 811
QY 306 MALEIQDRASV-----IKGAPVVEPS--NKEFWHRPDMVLFPIHLLTFQNAFO 352
DB 812 YLFSL-DOSTIQLTFVYLFLEFFFAKVSQTTWTYFWEFRSLKDKVFIK-NLFNDNFN 869
QY 353 MAHFVATVATPGLKCFHMHIGSLIKKVVGLALQELCSYTFPLVALYVQSGSNMKRSI 412
DB 870 SQWKIDLESSLVFIIFLIISGFNF---GIDNF--NLVIFLLAIY-----GL 914
QY 413 FDEQTA-----KALTNW-----RNTAKEKK-KVRDPTMLAAQMI 445
DB 915 FVAVATAFLPMFCFGLINGWLSPPNVVSHLSLKRKKHFKFIDIEOLI 964

RESULT 13
TRP DROME STANDARD: PRT: 1275 AA.
ID TRP DROME P19334.
AC 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transient receptor potential protein.
GN TRP.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=90180449; PubMed=2516726;
RA Montell C., Rubin G.M.;
RT "Molecular characterization of the Drosophila trp locus: a putative
RT integral membrane protein required for phototransduction.";
RL Neuron 2:1313-1323(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148782; PubMed=2482778;
RA Wong F., Schaefer E.L., Roop B.C., Lamendola J.N., Johnson-Season D.,
RA Shao D.;
RT "Proper function is important for normal visual transduction in the
RT development of the Drosophila trp gene product during pupal
RT adult.";
RL Neuron 3:81-94(1989).
RN [3]
RP SEQUENCE OF 1126-1275 FROM N.A.
RX MEDLINE=88042982; PubMed=3118483;
RA Wong F., Yun Z.T., Schaefer E.L., Roop B.C., Ally A.H.;
RT "Overlapping transcription units in the transient receptor potential
RT locus of Drosophila melanogaster.";
RL Somat. Cell Mol. Genet. 13:661-669(1987).
CC -1- FUNCTION: REQUIRED FOR PHOTOTRANSDUCTION. SUGGESTED TO MEDIATE
CC CALCIUM ENTRY. SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT
CC CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC

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CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC -----
DR EMBL: M34394; AAA28976.1; -
DR EMBL: M21306; AAA56928.1; -
DR EMBL: M18634; AAA28977.1; -
DR PIR: J00092; J00092.
DR PIR: J00015; J00015.
DR Flybase: FBgn0003861; trp.
DR InterPro: IPR002110; Ank_channel_TrpL.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR002153; Trans_recep.
DR InterPro: IPR004729; Trp_Cachannel.
DR Pfam: PF00023; ank; 3.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR01097; TRANSRECEPTR.
DR SMART: SM00248; ANK; 1.
DR TIGRfams: TIGR00870; trp; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REGION; 1.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW Vision; ANK repeat; Repeat.
FT DOMAIN 1 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 387 POTENTIAL.
FT DOMAIN 388 390 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 391 411 POTENTIAL.
FT DOMAIN 412 418 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 419 439 POTENTIAL.
FT DOMAIN 440 450 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 451 471 POTENTIAL.
FT DOMAIN 472 507 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 508 528 POTENTIAL.
FT DOMAIN 529 541 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 542 562 POTENTIAL.
FT DOMAIN 563 638 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 639 659 POTENTIAL.
FT DOMAIN 660 1275 EXTRACELLULAR (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 143 172 ANK 2.
FT CONFLICT 285 288 GORO -> ASSE (IN REF. 2).
FT CONFLICT 326 329 RRKO -> POE (IN REF. 2).
FT CONFLICT 365 374 KPFVKFTHS -> NPLSSSSRRP (IN REF. 2).
FT CONFLICT 785 785 S -> N (IN REF. 2)
SQ SEQUENCE 1275 AA; 142589 MW; 91CFCDD9896989B1 CAC64;

Query Match 3.7%; Score 103.5; DB 1; Length 1275;
Best Local Similarity 18.3%; Pred. No. 1.9;
Matches 133; Conservative 87; Mismatches 235; Indels 271; Gaps 29;

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DB 254 GTSLDHATNSMELEVMNHNHPSHDIMCLOGROTLERLKAIRYKOTCFVAPWQOL 313
QY 206 VAE-----FROEFSYVRKVDYLLLRAG-----INAHSHNSKF---DEHKYIKR 247
DB 314 LAAIWYDGLPGRRKQASQOOLMDVNLGCSFPIYSIKYILAPDSEGAKEFRKPFVKFIH 373
QY 248 SMEDDFV-----VGISLPL-----WCVAAIL----- 269
DB 374 SCGYMFLMLLGAASLRYVQITFELLAFAPMMLTLEDNRKHERGSLPGIELAITYIMA 433
QY 270 -----TLFID-----IDGIGTWISPIPLVILGCKLEMTIMEALEI 310
DB 434 LIFEELKSLYSDGLEFYIMDLNINVDISMRVTWI-----LCRAI-----AWVI 479
QY 311 QDRASVYKGAPEVPSNKFWEHPRDM----- 337
DB 480 VHRDLNFRG---IDP-----YFPREHHPEDPMLTSEGAFAAGVFSYKLVIHFIINPH 531
QY 338 -----VLEFTH-LTLEQNAFOAHFVMTVATPGLKCFEHH----- 372
DB 532 LGPLQVSLGRMTIIDIKFFIYTLVLFARCGGLNQLMRYALEKNKCYHLHPDVADDFD 591
QY 373 -----IGLSIMKVVIGL-----ALQFLCSTITPPLY 398
DB 592 QEKACTIMRFRSNIFFETQSILFMASFGILDVLSFDLAGIKSFTRFMALMFGSYVINII 651
QY 399 ALVTONGSMKRSIFDEQTAKALFNMRNTAKKVKVBDTDLMAOMIGDAPTSRGTSPMP 458
DB 652 VILNMLIAMSNS-YQIISEADTEWK-----FARSDLMKSYFDEGGITLPP 697
QY 459 SRASSVHLHKMGSRDDPOSAPTSPTIMEARMDYPPVYVAHPYHLINPADRRSVSS 518
DB 698 FNLCPMKMLRTKLRKPRSTKSEMRKSMERAQTLHDKVMLVRRYITAEQRDDYG 757
QY 519 ALDADI 524
DB 758 ITEDDI 763

RESULT 14
ID GPR1_RAT STANDARD: PRT; 353 AA.
AC P46090;
DE 01-NOV-1995 (Rel. 32, Created)
DE 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Probable G protein-coupled receptor GPR1.
GN Rattus norvegicus (rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95110347; PubMed=7811287;
RA Marchese A., Cheng R., Lee M.C., Porter C.A., Helber M., Goodman M.,
RA George S.R., O'Dowd B.F.;
RT "Mapping studies of two G protein-coupled receptor genes: an amino
RT acid difference may confer a functional variation between a human and
RT rodent receptor."
RL Biochem. Biophys. Res. Commun. 205:1952-1958(1994).
CC -1- FUNCTION: ORPHAN RECEPTOR. PROBABLE OPIOID RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC EMBL: S74702; AAB32978.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PR00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 42 62 1 (POTENTIAL).
FT DOMAIN 63 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 94 2 (POTENTIAL).
FT DOMAIN 95 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 231 5 (POTENTIAL).
FT DOMAIN 232 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 268 6 (POTENTIAL).
FT DOMAIN 269 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 307 7 (POTENTIAL).
FT DOMAIN 308 353 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
SQ SEQUENCE 353 AA; 40901 MW; 8C526CB5C74087A CRC64;

Query Match
Best Local Similarity 20.5%; Score 98; DB 1; Length 353;
Matches 81; Conservative 55; Mismatches 115; Indels 144; Gaps 21;

QY 111 DYCAKRGKVSLSMSTGSLHQLHIFVLA-VFHVYSVIALMSRLKRTWKKEETAS 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 20 EYXSQPDAAEENVYGIYHWSLILYALFVLGIPNALVIMFEK---WKKVITLM 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 170 LEYQFANDPARREFTHQSFYKRLGLS-STPGIRVV---AFNQ-----FRRSVK 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 LNLALD---FIFVLEPLYSIVALSFWPGNMLCKLNSFIQLQNMSSVEFLTVIS 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 VD-YLTLAGFTNAHLSNKSDFHKYKSMEDKRVVGSISPLMCAVL---TLF- 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 LDRYIHL---IHPGLSHP-----HRTLKNSL---LVV---LEVMLASLGGPTLYE 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 273 -----LDIDIGISLTWISF-----IPVYL---LCV---GRTLEK 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 176 RDVEYVNNIIICYNNFQYELTLRHNVLTWVAFLEGYLLPLWSSCYCLLFKTKKON 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 IINEMALEIQDRASYIKGAPVPEPSNKFV-----FRR-PDWVLFTHLT 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 236 ILL-----SSKHLMLILSVIAFVNCWTFPHLSIMELSIHNS 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 LFQNAFQMAHFVTVATPGLKCFPHMHIGLSIMKVVGLAIOFCSYTTPFLVALYQ-- 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 275 SFQNVLDGS-----IPLSGLAFLNSCLNPLLYIISKRF 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 404 -----MGSNKSISDEQTAALINMNTAKK 431
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 310 QARFASVAEVLKSLWEASCSGTVEOLSAETK 344
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
YHGE_ECOLI
ID YHGE_ECOLI STANDARD; PRT; 574 AA.
AC P45804;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yhge.
GN YHGE OR B3402.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-9742617; Pubmed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: SOME, TO B.SUBTILIS YRDE.
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CC
DR EMBL: U18997; AAB58199.1; -.
DR EMBL: AE000415; AAC76427.1; -.
DR Ecogene: EG12931; Yhge.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 12 32 POTENTIAL.
FT TRANSMEM 39 59 POTENTIAL.
FT TRANSMEM 66 86 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 142 162 POTENTIAL.
FT TRANSMEM 178 198 POTENTIAL.
FT TRANSMEM 214 234 POTENTIAL.
FT TRANSMEM 248 268 POTENTIAL.
FT TRANSMEM 286 306 POTENTIAL.
FT TRANSMEM 320 340 POTENTIAL.
FT TRANSMEM 373 393 POTENTIAL.
SQ SEQUENCE 574 AA; 64637 MW; 529E33C38D5BEF59 CRC64;

Query Match
Best Local Similarity 22.5%; Score 98; DB 1; Length 574;
Matches 68; Conservative 46; Mismatches 88; Indels 100; Gaps 16;

QY 120 VLSMSTGSLHQLHIFVLA-VFHVYSVIALMSRLKRTWKKEETAS 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 53 VLSFSVLSFQKRLMGWALVF-----IATLMSGMLKWTQDGNPRAEAKALMD 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 Y-----QFANDPARREFTHQSF--VKRHIGSSTPGIRVV-----ETASLE 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 103 FGCYLLAMALLPWIQSLRIRNDSRRFRFYGSVHNVLILVIFLANGLTWLVLLM 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 -----AFFQFRSVTKVDYLTLAGFINA-----HLSNKSDFHKYKSMEDD 252
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 163 SELFKLVGITFEFTLPFAIDWPIYVLT--GLVTLAVILARTOSRLD-----SIKRL 213
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 253 FKVVVGISLPLMCVAITLTF---LDIDIGISLT-WISFTPLVILCVGTEKLEMTIMMA 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 214 FTLIATGLPLP--VSLITLMEITITLPTGLSISRHSIAGGLLTTLAF--LQILMIV 268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 LEIQDRAS-----VIKGAPVPEPSNKFVRRDWLFFTHLTLEQNAFQMAHFV 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 269 RDPQ-KASLWPTGRLCLIKTALVAPLYEV-----AAMALW-----LRVAQYGW 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 359 TV 360
   : :
DB 314 TV 315
```

Search completed: November 18, 2002, 15:36:53
Job time : 28 secs

...

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 15:32:23 ; Search time 81 Seconds

(without alignments)
1358.385 Million cell updates/sec

Title: US-09-857-896A-32

Sequence: 1 MADDDEYPPARTLPETPSMA.....VSSSALDADIPSADEFSQG 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PLANT:*
10: SP_PODENT:*
11: SP_VIRUS:*
12: SP_VIRUS:*
13: SP_VIRUS:*
14: SP_VIRUS:*
15: SP_VIRUS:*
16: SP_VIRUS:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2736	98.3	534	10	094FR4
2	2718	97.6	534	10	094FR1
3	2681	96.3	534	10	094FR2
4	2205	79.2	435	10	094FR3
5	2036.5	73.2	555	10	095NKS
6	2033.5	73.0	555	10	095NKS
7	1875	67.3	554	10	094KX8
8	1755	63.0	563	10	094CH4
9	1281.5	46.0	576	10	094KX3
10	1276.5	45.9	573	10	095YB6
11	1241	44.6	583	10	095Y94
12	1228	44.1	583	10	094KX7
13	1213.5	43.6	580	10	095Y94
14	1201	43.1	515	10	094KX3
15	1195	42.9	565	10	094KX3
16	1160.5	41.7	569	10	095Y94

17	1149.5	41.3	593	10	095HMO
18	1100.5	39.5	467	10	095HMO
19	1058	38.0	443	10	095HMO
20	1012	36.4	508	10	094KX9
21	912	32.8	339	10	094KX4
22	888	31.9	492	10	094KX7
23	886.5	31.8	406	10	094KX6
24	886	31.8	478	10	094KX2
25	860.5	30.9	429	10	095Y94
26	841	30.2	171	10	094KX8
27	838.5	30.1	485	10	094KX8
28	796.5	28.6	496	10	094KX2
29	796	28.6	554	10	094KX1
30	780	28.0	573	10	095Y94
31	770.5	27.7	499	10	094KX8
32	741	26.6	509	10	094KX1
33	715	25.7	573	10	094KX8
34	641.5	23.0	507	10	094KX2
35	607.5	21.8	469	10	094KX6
36	606.5	21.8	311	10	094KX5
37	269	9.7	103	10	094KX2
38	260	9.3	77	10	094KX4
39	257.5	9.2	78	10	094KX9
40	257.5	9.2	78	10	094KX4
41	253.5	9.1	78	10	094KX5
42	252	9.1	77	10	094KX4
43	252	9.1	77	10	094KX4
44	252	9.1	77	10	094KX2
45	250.5	9.0	78	10	094KX6

ALIGNMENTS

RESULT 1

ID	Q94FR4	PRELIMINARY:	PRT:	534 AA.
AC	Q94FR4;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
GN	Seven transmembrane-spanning protein.			
OS	Triticum aestivum (Wheat).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;			
OC	Triticaceae; Triticum.			
OX	NCBI_Taxid=4565;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-CV. BOB WHITE;			
RA	Devoto A., Hartmann A., Piffanello P., Elliott C., Simmons C.,			
RA	Taramino G., Goh C.-S., Schulze-Lefert P., Panstruga R.;			
RT	"Co-Evolution among Intracellular domains and the C-terminus of the			
RT	seven-transmembrane M10 protein is suggested by a detailed			
RT	computational analysis."			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF361932; AAK94904.1; -			
DR	InterPro: IPR004326; M10.			
DR	Pfam: PF03094; M10; 1.			
KW	Transmembrane.			
SQ	SEQUENCE 534 AA; 60427 MW; 2DB2384078336D00 CRC64;			

Query Match 98.3%; Score 2736; DB 10; Length 534;
Best Local Similarity 97.9%; Pred. No. 9.7e-250;
Matches 523; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY	1	MADDDEYPPARTLPETPSMAVAFVAVVIVVLEHMLHGLGHWFFKRRKRLNALALEK 60
DB	1	MADDDEYPPARTLPETPSMAVAFVAVVIVVLEHMLHGLGHWFFKRRKRLNALALEK 60
QY	61	IKAEILMGFTSLLAATODPISGICISERKASINRPSCLPPGSKYSKYDYCAKRGV 120

Db 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPACKLPGSVSKSYKDYCYCAKQKV 120
QY 121 SLMTSGSLHGHIFIFVLAVFHTYTSVITMALSRKMTWKMTETASLETOFANDPAR 180
Db 121 SLMTSGSLHGHIFIFVLAVFHTYTSVITMALSRKMTWKMTETASLETOFANDPAR 180
QY 181 FRFHQTSFVKRHLGLSTPGIRWVAVFEPFQFRRSVTKVDYLTLAGFTINHLSHNSKED 240
Db 181 FRFHQTSFVKRHLGLSTPGIRWVAVFEPFQFRRSVTKVDYLTLAGFTINHLSHNSKED 240
QY 241 FHKYIKRSMEDDEKVVVIGSLPLWCVAITLFLDIDIGITLWTSFPLVILLCVGTKLE 300
Db 241 FHKYIKRSMEDDEKVVVIGSLPLWCVAITLFLDIDIGITLWTSFPLVILLCVGTKLE 300
QY 301 MIEMALEIODRASVIGAPVVEPSNKFEPHFRPDVWLFETHLTLPONAFQMAHFVWTV 360
Db 301 MIEMALEIODRASVIGAPVVEPSNKFEPHFRPDVWLFETHLTLPONAFQMAHFVWTV 360
QY 361 ATPGKLCFPMHIGLSIMKVVLGLALQFLCSYITPFLYALVTOMSNKRSIFPEOTAKA 420
Db 361 ATPGKLCFPMHIGLSIMKVVLGLALQFLCSYITPFLYALVTOMSNKRSIFPEOTAKA 420
QY 421 LTNMRNTAKKKVRYDMDLMAOMIGDATPSRGTSPMPSRASSPVHLHKMGSRDDPOS 480
Db 421 LTNMRNTAKKKVRYDMDLMAOMIGDATPSRGTSPMPSRASSPVHLHKMGSRDDPOS 480
QY 481 APTSPRTMEARMDYPVYVAHPVHRLNPADRRRSVSSALDDIPSDAFSFSOG 534
Db 481 TPTSPRAMEARMDYPVYVAHPVHRLNPADRRRSVSSALDDIPSDAFSFSOG 534

RESULT 2

Q94F71 PRELIMINARY; PRT; 534 AA.
ID 094F71
AC 094F71;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MLo1 protein.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
RT "Cloning, characterization analysis and expression of MLo1 gene from
RT wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF384145; AAK60567.1; -;
DR InterPro: IPR004326; MLo.
DR Pfam: PF03094; MLo; 1.
SQ SEQUENCE 534 AA; 60402 MW; 7CB186B64F3C5E66 CRC64;

Query Match 97.6%; Score 2718; DB 10; Length 534;
Best Local Similarity 97.6%; Pred. No. 4,96-248;
Matches 521; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MAEDYEPPARTLPETPSMAVALVFAVMIIVSVLLEHALHKGHFHRRKRNALAEALER 60
Db 1 MADDEYPPARTLPETPSMAVALVFAVMIIVSVLLEHALHKGHFHRRKRNALAEALER 60
QY 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPACKLPGSVSKSYKDYCYCAKQKV 120
Db 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPACKLPGSVSKSYKDYCYCAKQKV 120
QY 121 SLMTSGSLHGHIFIFVLAVFHTYTSVITMALSRKMTWKMTETASLETOFANDPAR 180
Db 121 SLMTSGSLHGHIFIFVLAVFHTYTSVITMALSRKMTWKMTETASLETOFANDPAR 180
QY 181 FRFHQTSFVKRHLGLSTPGIRWVAVFEPFQFRRSVTKVDYLTLAGFTINHLSHNSKED 240
Db 181 FRFHQTSFVKRHLGLSTPGIRWVAVFEPFQFRRSVTKVDYLTLAGFTINHLSHNSKED 240

Db 181 FRFHQTSFVKRHLGLSTPGIRWVAVFEPFQFRRSVTKVDYLTLAGFTINHLSHNSKED 240
QY 241 FHKYIKRSMEDDEKVVVIGSLPLWCVAITLFLDIDIGITLWTSFPLVILLCVGTKLE 300
Db 241 FHKYIKRSMEDDEKVVVIGSLPLWCVAITLFLDIDIGITLWTSFPLVILLCVGTKLE 300
QY 301 MIEMALEIODRASVIGAPVVEPSNKFEPHFRPDVWLFETHLTLPONAFQMAHFVWTV 360
Db 301 MIEMALEIODRASVIGAPVVEPSNKFEPHFRPDVWLFETHLTLPONAFQMAHFVWTV 360
QY 361 ATPGKLCFPMHIGLSIMKVVLGLALQFLCSYITPFLYALVTOMSNKRSIFPEOTAKA 420
Db 361 ATPGKLCFPMHIGLSIMKVVLGLALQFLCSYITPFLYALVTOMSNKRSIFPEOTAKA 420
QY 421 LTNMRNTAKKKVRYDMDLMAOMIGDATPSRGTSPMPSRASSPVHLHKMGSRDDPOS 480
Db 421 LTNMRNTAKKKVRYDMDLMAOMIGDATPSRGTSPMPSRASSPVHLHKMGSRDDPOS 480
QY 481 APTSPRTMEARMDYPVYVAHPVHRLNPADRRRSVSSALDDIPSDAFSFSOG 534
Db 481 TPTSPRAMEARMDYPVYVAHPVHRLNPADRRRSVSSALDDIPSDAFSFSOG 534

RESULT 3

Q94F72 PRELIMINARY; PRT; 534 AA.
ID 094F72
AC 094F72;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MLo protein.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
RT "Cloning, location and expression of MLo gene from wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF384144; AAK60566.1; -;
DR InterPro: IPR004326; MLo.
DR Pfam: PF03094; MLo; 1.
SQ SEQUENCE 534 AA; 60298 MW; 6C9640E30FDE5189 CRC64;

Query Match 96.3%; Score 2681; DB 10; Length 534;
Best Local Similarity 96.1%; Pred. No. 1,5e-244;
Matches 513; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 MAEDYEPPARTLPETPSMAVALVFAVMIIVSVLLEHALHKGHFHRRKRNALAEALER 60
Db 1 MAKDDYPPARTLPETPSMAVALVFAVMIIVSVLLEHALHKGHFHRRKRNALAEALER 60
QY 61 IKAELMLVGFISLLAVTODPISGICISEKASIMRPACKLPGSVSKSYKDYCYCAKQKV 120
Db 61 IKAELMLVGFISLLAVTODPISGICISOKNASTMRCCYEGSVSKSYKDYCYCAKQKV 120
QY 121 SLMTSGSLHGHIFIFVLAVFHTYTSVITMALSRKMTWKMTETASLETOFANDPAR 180
Db 121 ALMTSGSLHGHIFIFVLAVFHTYTSVITMALSRKMTWKMTETASLETOFANDPAR 180
QY 181 FRFHQTSFVKRHLGLSTPGIRWVAVFEPFQFRRSVTKVDYLTLAGFTINHLSHNSKED 240
Db 181 FRFHQTSFVKRHLGLSTPGIRWVAVFEPFQFRRSVTKVDYLTLAGFTINHLSONSKED 240
QY 241 FHKYIKRSMEDDEKVVVIGSLPLWCVAITLFLDIDIGITLWTSFPLVILLCVGTKLE 300
Db 241 FHKYIKRSMEDDEKVVVIGSLPLWCVAITLFLDIDIGITLWTSFPLVILLCVGTKLE 300
QY 301 MIEMALEIODRASVIGAPVVEPSNKFEPHFRPDVWLFETHLTLPONAFQMAHFVWTV 360
Db 301 MIEMALEIODRSVIGAPVVEPSNKFEPHFRPDVWLFETHLTLPONAFQMAHFVWTV 360

QY 361 ATGCAKCFHMHGSLIMKVVGLALQFLCSYTFPLXALYTOMGSNNKRSITFEDQAKA 420
|||||
Db 361 ATGCAKCFHMHGSLIMKVVGLALQFLCSYTFPLXALYTOMGSNNKRSITFEDQAKA 420
QY 421 LTNWNTAKKKKKVBDTDLMAQMGATPSRGTSMPSPASSPVHLLHKMGSRDDPOS 480
|||||
Db 421 LTNWNTAKKKKKVBDTDLMAQMGATPSRGTSMPSPASSPVHLLHKMGSRDDPOS 480
QY 481 APTSPRTMEARDMYPVVAHPVHRLNADRRSSVSSALDDISADPSFSOG 534
|||||
Db 481 APTSPRTMEARDMYPVVAHPVHRLNADRRSSVSSALDDISADPSFSOG 534

RESULT 4

Q94FR3 PRELIMINARY; PRT; 435 AA.
ID Q94FR3
AC Q94FR3
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Seven transmembrane-spanning protein (Fragment).
GN MLO1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BOB WHITE;
RA Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.,
RA Taramino G., Goh C.-S., Schulze-Lefert P., Panstruga R.;
RT "Co-Evolution among intracellular domains and the C-terminus of the
RT seven-transmembrane MLO protein is suggested by a detailed
RT computational analysis."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361933; AAK94905.1; -
DR InterPro; IPR004326; MLO.
DR Pfam; PF03094; MLO; 1.
KW Transmembrane.
FT NON_TER
SQ SEQUENCE 435 AA; 49354 MW; 3D96BD52FA62D42B CRC64;

Query Match 79.2%; Score 2205; DB 10; Length 435;
Best Local Similarity 97.0%; Pred. No. 1.1e-193;
Matches 420; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 102 PGVSKSKYDYCAKKGKVSLSMSTGSLHQLHIFIFVLAVFHYTSVILMALSRKMTWK 161
|||||
Db 3 PGVSKSKYDYCAKKGKVSLSMSTGSLHQLHIFIFVLAVFHYTSVILMALSRKMTWK 62
QY 162 KWEETASLEXPANDPARFRFTHOTSPVKRHGLSSTGCIKWVAVAFRQFRSVTKVDY 221
|||||
Db 63 KWEETASLEXPANDPARFRFTHOTSPVKRHGLSSTGCIKWVAVAFRQFRSVTKVDY 122
QY 222 LTLRAGFINAHLSHNSKEDFNHYIKRSMEDDFKVVVGISLPLCAVAIITLFLDIDIGITL 281
|||||
Db 123 LTLRAGFINAHLSHNSKEDFNHYIKRSMEDDFKVVVGISLPLCAVAIITLFLDIDIGITL 182
QY 282 TWTSFTPIVYLLCVGKLEIMTMEALEIODRASVYIKGAPVPEPSNKKFFWHRDWWLFF 341
|||||
Db 183 TWTSFTPIVYLLCVGKLEIMTMEALEIODRASVYIKGAPVPEPSNKKFFWHRDWWLFF 242
QY 342 IHLTFQNAFQMAHFVWVAATPGALKCFHMHGSLIMKVVGLALQFLCSYTFPLXALY 401
|||||
Db 243 IHLTFQNAFQMAHFVWVAATPGALKCFHMHGSLIMKVVGLALQFLCSYTFPLXALY 302
QY 402 TOMGSNNKRSITFEDQAKALTNWNTAKKKKKVBDTDLMAQMGATPSRGTSMPSPASS 461
|||||
Db 303 TOMGSNNKRSITFEDQAKALTNWNTAKKKKKVBDTDLMAQMGATPSRGTSMPSPASS 362
QY 462 SSPVHLLHKMGSRDDPOSAPTSPRTMEARDMYPVVAHPVHRLNADRRSSVSSALD 521

Db 363 SSPVHLLHKMGSRDDPOSAPTSPRTMEARDMYPVVAHPVHRLNADRRSSVSSALD 422

QY 522 ADIPSADPSFSOG 534
|||||

Db 423 ADIPSADPSFSOG 435

RESULT 5

Q9SNK5 PRELIMINARY; PRT; 555 AA.
ID Q9SNK5
AC Q9SNK5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Similar to OsMLO-hl.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 3, PAC
RT clone:PO43E01."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000615; BAA85400.1; -
DR InterPro; IPR004326; MLO.
DR Pfam; PF03094; MLO; 1.
SQ SEQUENCE 555 AA; 62685 MW; F651FAD83B79E13C CRC64;

Query Match 73.2%; Score 2036.5; DB 10; Length 555;
Best Local Similarity 71.7%; Pred. No. 1.3e-183;
Matches 397; Conservative 46; Mismatches 70; Indels 41; Gaps 5;

QY 11 RLPEPTSMVAVALFAVMIIVSVLLEHALHKLGHMFHNRHKLALAELEKIKAEMLVGF 70
|||||
Db 8 RLPEPTSMVAVALFAVMIIVSVLLEHALHKLGHMFHNRHKLALAELEKIKAEMLVGF 67
QY 71 ISLLATVODPISIGTSEKASIMRPGSLPGSVK--SKYKV----- 112
|||||
Db 68 ISLLATVODPISIGTSEKASIMRPGSLPGSVK--SKYKV----- 112
QY 113 -----YAKKGVSLMSTGSLHQLHIFIFVLAVFHYTSVILMALSRKMTWK 163
|||||
Db 128 SLGAAGDEYCAQSGKVALMSGGMQLHIFIFVLAVFHYTSVILMALSRKMTWK 187
QY 164 ETEETASLEXPANDPARFRFTHOTSPVKRHGLSSTGCIKWVAVAFRQFRSVTKVDY 223
|||||
Db 188 ETEETASLEXPANDPARFRFTHOTSPVKRHGLSSTGCIKWVAVAFRQFRSVTKVDY 247
QY 224 LTLRAGFINAHLSHNSKEDFNHYIKRSMEDDFKVVVGISLPLCAVAIITLFLDIDIGITL 283
|||||
Db 248 MRQGFINAHLSONSKDFHNYIKRSMEDDFKVVVGISLPLCAVAIITLFLDIDIGITL 307
QY 284 ISFTPIVYLLCVGKLEIMTMEALEIODRASVYIKGAPVPEPSNKKFFWHRDWWLFF 343
|||||
Db 308 ISFTPIVYLLCVGKLEIMTMEALEIODRASVYIKGAPVPEPSNKKFFWHRDWWLFF 367
QY 344 LTLFQNAFQMAHFVWVAATPGALKCFHMHGSLIMKVVGLALQFLCSYTFPLXALY 403
|||||
Db 368 LTLFQNAFQMAHFVWVAATPGALKCFHMHGSLIMKVVGLALQFLCSYTFPLXALY 427
QY 404 MGSNNKRSITFEDQAKALTNWNTAKKKKKVBDTDLMAQMGATPSRGTSMPSPASS 463
|||||
Db 428 MGSNNKRSITFEDQAKALTNWNTAKKKKKVBDTDLMAQMGATPSRGTSMPSPASS 479
QY 464 PVHLLHKMGSRDDPOSAPTSPRTMEARDMYPVVAHPVHRLNADRRSSVSS 518
|||||
Db 480 PVHLLHKMGSRDDPOSAPTSPRTMEARDMYPVVAHPVHRLNADRRSSVSS 538

```
QY      519 ALDADIPSADFSS 532
          | : | | : | | | |
Db      539 AIQVDIADSDFFS 552
```

ID	Q93XCB	PRELIMINARY	PROT	555 AA
AC	Q93XCB			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Seven transmembrane protein MCO2.			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			
OX	NCBI_TaxID=4330;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. 1864; TISSUE=LEAF;			
RA	Devoto A., Hartman H.A., Piffenelli P., Elliott C., Simmons C., Taramino G., Goh C.-S., Cohen F.E., Schuler-Lefort P., Panstruga R.,			
RT	"Molecular phylogeny and domain-specific co-evolution of the plant-specific seven transmembrane MCO family."			
RL	Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF384030; AAK94907.1; -			
DR	InterPro: IPR004326; MCO.			
DR	Pfam: PF03094; MCO. 1.			
KW	Transmembrane.			
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Query Match	73.0%; Score 2033.5; DB 10; Length 555;			
Best local similarity	71.7%; Pred. No. 2,4e-183;			
Matches 397; Conservative 45; Mismatches 71; Indels 41; Gaps				
QY	11 RLPLEPSMAVALYPAVMITVSYLLEHALHLKLGWFEHKKRNALALEKIKAEITMLVGF 70			
DB	8 RALPEPTMAVAACVIAIVLYSVAMHEGHLKLGHWFEHKKRNALALEKIKAEITMLVGF 67			
QY	71 ISLLAVVQDDPSIGCISEKASIMPCSLPFGSVK--SKYKDY----- 112			
DB	68 ISLLVAVQDTPIKMICIPESANIMLPCAGODIVKGLKKKRRRLMLVGEESHRR 127			
QY	113 -----YAKGKGVSLMSTGSLQLHLIFPVLAAPHVITYSYITMALSLKMTKRW 163			
DB	128 SLAAGAGEDYCAQSGKVALMSSGGMHQLHIFPVLAAPHVITYSYITMALGRLKMKRW 187			
QY	164 ETEIASLEYOAPNPAFEFTHQTSFVKRHGLGSLSTFGIRMVVAFFRQFSRVTKVDLT 223			
DB	188 ELETNSLEYOAPNPSRFTHQTSFVKRHGLGSLSTFGIRMVVAFFRQFSRVTKVDLT 247			
QY	224 LRAGFINHLSHNSKPEFKYIKRSNEDDFKVVVIGSLPLMCVAILTLEPLDIDGIGTILW 283			
DB	248 MKRGFTNHLHSNSKPEFKYIKRSNEDDFKVVVIGSLPLMCVAILTLEPLDIDGIGTILW 307			
QY	284 ISFPIVLICVGRKLEMIIMMALIELIDRASVIKGAVPVPSNKEFFMHRPDWLEFIH 343			
DB	308 ISFVPIVLIMVGRKLEMIIMMAEIOIDRAVIKGAVPVPSNKEFFMHRPDWLEFIH 367			
QY	344 LTFPONAQOMAHFWATVATPGTKCKCHNHIGISIMKVVIALALQIFCSVTTPPLATVLTQ 403			
DB	368 LTFPONAQOMAHFWATVATPGTKCKCHNHIGISIMKVVIALALQIFCSVTTPPLATVLTQ 427			
QY	404 MGSNKRSLFDEQATAKLIMRNATAEKKKRVLDITMLMAOMIGDATPSRGTSPMFSRASS 463			
DB	428 MGSNKRSLFDEQATAKLIMRNATAEKKKRLDADDEFALQMSGDTTPSRG-----SS 479			
QY	464 PVHLHLHKGSGSDPOSAPSPPTMEEARADWYPVVVA-----HPVRLPADRRRRSSSS 518			
DB	480 PVHLHLHKGVRSEDPSPAPSPGFCAGARDMTVPVPAVPVRPGFNKIDP-DKRRASSSS 538			
QY	519 ALDADIPSADEFSFS 532			

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Db      539 AIQVDIADSDSFS 552
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Q3	Q3	Q3	100	100	0.0	100	100	100	0
Q4	Q4	Q4	100	100	0.0	100	100	100	0
Q5	Q5	Q5	100	100	0.0	100	100	100	0
Q6	Q6	Q6	100	100	0.0	100	100	100	0
Q7	Q7	Q7	100	100	0.0	100	100	100	0
Q8	Q8	Q8	100	100	0.0	100	100	100	0
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Q10	Q10	Q10	100	100	0.0	100	100	100	0
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Q16	Q16	Q16	100	100	0.0	100	100	100	0
Q17	Q17	Q17	100	100	0.0	100	100	100	0
Q18	Q18	Q18	100	100	0.0	100	100	100	0
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Q41	Q41	Q41	100	100	0.0	100	100	100	0
Q42	Q42	Q42	100	100	0.0	100	100	100	0
Q43	Q43	Q43	100	100	0.0	100	100	100	0
Q44	Q44	Q44	100	100	0.0	100	100	100	0
Q45	Q45	Q45	100	100	0.0	100	100	100	0
Q46	Q46	Q46	100	100	0.0	100	100	100	0
Q47	Q47	Q47	100	100	0.0	100	100	100	0
Q48	Q48	Q48	100	100	0.0	100	100	100	0

Db 424 VALYQMGTSKRPITFNDRYANLAKMHHHTAKQTKHGS-----GSNTPHSSRPT 475
Qy 458 PSRRASPVHLHLKMGSRDDPO-----SAPTSPRTMEKRDMPYVAHPRHLNRPADRR 513
Db 476 PTHGMSPVHLHLNHNRSDDQTSFTASPSRPESDYSGGCH-----GHQ-HFFPDSONH 530
Qy 514 SVSSSALDADI-----PSADFS 530
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RESULT 10
Q9SXB6
ID Q9SXB6 PRELIMINARY; PRT; 573 AA.
AC Q9SXB6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE T28B6.4 protein (Membrane protein M102).
GN T28B6.4
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federici N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buchler E., Dunn P.,
RA Gonzalez A., Kremetska I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Devoto A., Hartman H.A., Piffaneli P., Elliott C., Simmons C.,
RA Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
RT specific seven transmembrane M10 family".
RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC007259; AAD4991.1; -.
DR EMBL; AF369563; AAK53795.1; -.
DR InterPro; IPR004326; M10.
DR Pfam; PF03094; M10; 1.
SQ SEQUENCE 573 AA; 65543 MW; 36FA911F8BD9A46 CRC64;

Query Match 45.9%; Score 1276.5; DB 10; Length 573;
Best Local Similarity 48.8%; Pred. No. 8.3e-112;
Matches 251; Conservative 76; Mismatches 142; Indels 45; Gaps 4;
Qy 11 RTLPETPSMAVALFAVAMITVSYLEHLAKLGHMFHRRHKNALAELEKIKALMLVGF 70
Db 8 RLEETSTMAVAVCFVLFTISYLESHSIHKIGTWFKKKHKALEKIKALMLLGF 67
Qy 71 ISLLAVTODPISGICISEKAASIMRCSLPPGSVKSXYKDY----- 112
Db 68 ISLLLTIGOTPLSNICISOKVASTMPCSAAEAKYKKAKGAKGDDGDKGRLLIE 127
Qy 113 -----YCAKKGVSIMSTGSLHQLHIFVLAVFHTYSVILMALSL 155
Db 128 LAESYIHRSLATKGYDKCAEKGVAFVSAIGIHIFVLAVVAVVCIYATYAFGI 187
Qy 156 KRRYKKMETETASLETOFANDPARFRFHOTSFPVKNHIGL-SSTPGIRMVAVFFQOPR 214
Db 188 KRRYKSNBEETKTIETQYSNDPERFRFARDTSFGRRLLNWSSTRVTLTIYVFFQOPR 247
Qy 215 SVTKVYDLTLRAGFINAHL-S-HNSKDFHKYIKRSMDEDFKVVVGLSLMCVALITLF 272
Db 248 SVTKVYDLALRHGFIMAHFAPGNESRFDRKTIQSLKDKYVEISPIYMFVAVLFL 307
Qy 273 LDIDIGTLTWISFTPIVILLCVGTKLEMIEMALEIQQDASVIKAPVYESNKFYFHR 332
Db 308 TNSYGRSLYMLPFIPLVILIVGTLEVIITKGLRIQEKGDVVGAPVVGDDLEFWE 367

Qy 333 HRPDWVLEFHLITLQONAFOMAHFVMTVATPGLKCFHMHGILSNKVGLALQFLCSY 392
Db 368 GKRFELIFLHLIVFTNFAFOLAFRANSTYEPNLNNGHSTADVIRLVAVVQILCSY 427
Qy 393 ITPPLVALYTOGMSNKRISIFDEOTAKALTNMKNYKKEKKYKRDPMIMAOITDAPSR 452
Db 428 VTLPLVALYTOGMSKKKPTVFNDRVATLAKMHHHTAKNETK-----HGRHSNTSPFS 480
Qy 453 GTSMPSPRASPVHLHLKMGSRDDPOSAPTSPR 486
Db 481 SRPTTPRHGSSPHLHLNPNRNVENYTPSSPSPR 514

RESULT 11
Q9SY94
ID Q9SY94 PRELIMINARY; PRT; 583 AA.
AC Q9SY94;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE T25B24.9 protein.
GN T25B24.9
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federici N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buchler E., Dunn P.,
RA Gonzalez A., Kremetska I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC005850; AAD25552.1; -.
DR InterPro; IPR004326; M10.
DR Pfam; PF03094; M10; 1.
SQ SEQUENCE 583 AA; 67226 MW; 6EA3683CA8BB9150 CRC64;

Query Match 44.6%; Score 1241; DB 10; Length 583;
Best Local Similarity 47.6%; Pred. No. 1.9e-108;
Matches 247; Conservative 86; Mismatches 138; Indels 48; Gaps 6;
Qy 11 RTLPETPSMAVALFAVAMITVSYLEHLAKLGHMFHRRHKNALAELEKIKALMLVGF 70
Db 8 KLEETSTMAVAVCFVLFTISYLESHSIHKIGTWFKKKHKALEKIKALMLLGF 67
Qy 71 ISLLAVTODPISGICISEKAASIMRCS----- 99
Db 68 ISLLLTIGOOTPLSNICIPKNTIAASWPCSAEERARYGKDDVPKDEEENLRKLQDLV 127
Qy 100 --LPPGSVKSXYKDYCAKKGVSIMSTGSLHQLHIFVLAVFHTYSVILMALSLMK 157
Db 128 SLIPRRLAKGID-KCAEKGVAFVSAIGMHQLHIFVLAVCHVCIYATLALGKTM 186
Qy 158 RTWKKMETETASLETOFANDPARFRFHOTSFPVKNHIGLSSPTGIR-VVAVFFQOPRSY 216
Db 187 RRRKKMEETKTIETQYSNDPERFRFARDTSFGRRHLSFWSKSTITLTIYVFFQOPRSY 246
Qy 217 TKVYDLTLRAGFINAHLNHS--KFDFFHKYIKRSMDEDFKVVVGLSLMCVALITLFLD 274
Db 247 TKVYDLTLRAGFINAHLAPGSAARDPKRTIQLSDEDKTIYELNPYIYINAVLFLTN 306
Qy 275 IDIGTLTWISFTPIVILLCVGTKLEMIEMALEIQQDASVIKAPVYESNKFYFHR 334
Db 307 TNGNSYMLWPFIFPIVILIVGTQYIITKGLRIQEKGDVVGKSTPLVOPGDHFFWFG 366
Qy 335 PDWVLEFHLITLQONAFOMAHFVMTVATPGLKCFHMHGILSNKVGLALQFLCSYT 394
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QY 395 FPLVALVTOMGSMKRSIFDEQAKALTLNWRNTAKKKVYROTDMLAQMIGATPSRGT 454
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DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Membrane protein M106.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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RA Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA Tarantino G., Goh C., Cohen F.E., Schulze-Isferl P., Panstruga R.,
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
RT specific seven transmembrane M10 family."
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF369567; AAK53799.1; -.
DR InterPro: IPR004326; M10.
DR Pfam: PF03094; M10; 1.
SQ SEQUENCE 583 AA; 67097 MW; 4DA8683CA8BC5C5D CRC64;
Query Match 44.1%; Score 1228; DB 10; Length 583;
Best Local Similarity 47.4%; Pred. No. 3.2e-107;
Matches 246; Conservative 86; Mismatches 139; Indels 48; Gaps 6;
QY 11 RTLPETPSMAVALVFAVMIVSVLELALHKLGHWFKRHKNALEALEIKALMLVGF 70
Db 8 KTLDETSMAVAVCFVLLSLIVLELHKIGSGFKKKNALEYELKAKELMLMGF 67
QY 71 ISLLAVTODPSIGICISEKAASIMRPS-----KDYCC 114
Db 68 ISLLTIGGYISNICIPKNIAASMHPCASSEARKYCKKDVPEDEENLRKLLQLYD 127
QY 100 --LPGSVKSKKYDYCAKKGKYSLSQHLIFIVLAVFHVTVSVIINALSLRLM 157
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QY 275 IDIGTLTWISFIPVLVILLCVGTLEMIEMALEIODRASVINGAVPSPSKFFWHR 334
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QY 395 FPLVALVTOMGSMKRSIFDEQAKALTLNWRNTAKKKVYROTDMLAQMIGATPSRGT 454
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QY 455 SPMPSSRASSPVHL-----HKMGSRDDPOSAPTSPTTME 489

Db 480 PTPPTHGSSPIHLRNAPHKRSVDESFANSPSRNSD 518
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AC 09FRJ3:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative M10 (pathogen resistance) protein.
GN OSJNB0064P21.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocarpaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N. A.
RA STRAIN-CV. NIPPONBARE.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zisman V., Pal G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
RT "Oryza sativa chromosome 10 BAC OSJNB0064P21 genomic sequence."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC073166; A646114.1; -.
DR InterPro: IPR004326; M10.
DR Pfam: PF03094; M10; 1.
SQ SEQUENCE 580 AA; 64796 MW; CD263AD8F8C350FC CRC64;
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Best Local Similarity 46.5%; Pred. No. 7.6e-106;
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QY 175 ANDPARFRTHTQTSFVKRHGLSSTPGIRWVAVFFROPFRSVTKVDYTLTRAGFINAHL 233
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QY 414 DEQAKALTLNWRNTAKKKVYROTDMLAQMIGATPSRGTSPMPSSRASS----- 463
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QY 464 -PVHLTK-----GMGRSDPOSAPTSPTTMEARWYVYVAHVHNLNADRRS 514
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Db 427 AKALKKKHKAAYKKKKHKDSHNSF-----TPSIDTTGPAGEGEWORLDHEVYVRLHR 481
QY 471 -----GMSRSDDPQAP-----TSPRTMEEARDMYPVVAHPVHRLNPADRRRSYSSS 518
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Search completed: November 18, 2002, 15:38:34
Job time : 83 secs

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TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
REFERENCE Unpublished (2002)
AUTHORS 2 (bases 1 to 1812)
Coe, E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES Location/Qualifiers
source 1. 1812
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/db_xref="maizedb:632910"
/db_xref="taxon:4577"
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/clone_lib="Maize Mapping Project/Dupont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 341 a 468 c 430 g 384 t 189 others
ORIGIN

Alignment Scores:
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Score: 1202.00 Matches: 266
Percent Similarity: 55.818 Conservative: 46
Best Local Similarity: 47.588 Mismatches: 98
Query Match: 43.188 Indels: 150
Gaps: 7

US-09-857-896A-32 (1-534) x AY110401 (1-1812)

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Db 18 CAGGCAAGGTGTCCTCCATCTCTCGGCCGCGCCACCAAGCATCTTCATCTTC 77
QY 137 ValLeuAlaValPheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLys 156
Db 78 GTGCTCGCGGTTCATATCGCTACAGCGTCCGCCACCATGGCGCTGCTNNNN 137
QY 157 MetArgThrTrpLysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPheAlaSn 176
Db 138 NNN 197
QY 177 AspProAlaArgPheArgPheThrHisGlnThrSerPheValLysArgHisLeuGlyLeu 196
Db 198 GACCTTCACGGTTCGCGTTCACGACCAAGCATGTCGTTCGTAAGCGGACCTGGCCTC 257
QY 197 SerSerThrProGlyIleArgTrpValVal----- 206
Db 258 TCGACACCCCTGAGAGTGAATGGTCTGAGTACTCGACGAGATCGCACGCTTTTGA 317
QY 206 ----- 206
Db 318 GCCGTGCTATCGTTAAGTTCTCCGCCCTGGTTTATAGCCTAGGCTCTGNNNNNN 377
QY 207 -----AlaPhePheArgGlnPhePheArgValThrLys 218
Db 378 NNN 437
QY 218 sValAspTyrIleuThr----- 223
Db 438 GGTGGATTACCTGACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 497
QY 223 ----- 223
Db 498 TTGTTAATATGCTATGTGTGACTGGTATGATTCGCTAAGCCTTTTATGCTGTGACACGGC 557
QY 224 -----LeuArgAlaGlyPhe-IleAsnAlaHisLeuSerHisAsnSerLysPheAspPhe 242

Db 558 GATGTCGTGCTTGCTTCTCTCGACATGACATCTGCTCCGACACCAAGTCACTTGC 617
QY 242 IsLysTrpIleLeuArgSerMetGlnAspAspPheLysValValValGlyIleSerLeuP 262
Db 618 AGCAGTACATCAAGGGGCTCTGGAGAGACACTTCAAGATGCTGCTGGCATAGCTTC 677
QY 262 roLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAspGlyIleGlyThrLeu 282
Db 678 CGCTGGGTCTGCTCCCATCTTCATCTGTATGATATCAAGGATTCGGACCGCTTG 737
QY 282 hrTrpIleSerPheIleProLeuVal----- 290
Db 738 TCTGGATCTCTTTTGTCCCGCTCGT-TGTAAGGTTCAGAGCCATCGTCTGCTTTTA 796
QY 290 ----- 290
Db 797 GTTTTCTAGACACATCCCTATATGCTGCTGCTCCGCTGTTGGACAGACAAAGAC 856
QY 290 ----- 290
Db 857 CAATTGCTATTCACAAAACAGATCCAGCTTAAACCCCTTGGAATTATGTAATCTACA 916
QY 291 -----IleLeuLysCysValGlyThrLysL 299
Db 917 GTATAGTATACAAAGCGCTGCTGTGTTCAGTATCTCTCTGATGTTGGGCCCAAGC 976
QY 299 euGluMetIleIleMetGluMetAlaLeuGluIleGlnAspArgAlaSerValIleLysG 319
Db 977 TGGAGTTCATCTATGAGATGAGTGGCCACAGATACAGACAGCGATCATCAANN 1036
QY 319 lValAlaProValAlaGluProSerAsnLysPheThrPheHisArgProAspTrpValL 339
Db 1037 NNNCGCCGCTGTGAGCAAGTACAGCTTCTTGTTAACCGCCCTGGCTGGANN 1096
QY 339 euPhePheIleHisLeuThrPheGlnAsnAlaPheGlnMetAlaHisPheValTrpT 359
Db 1097 NNN 1156
QY 359 hrValAlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIleMetL 379
Db 1157 CACTGTCACCCCAACCTCAAGAAATGCTACACACAGAGGTGGGCTTGAGCATATCA 1216
QY 379 sValAlaLeuGlyLeuAlaLeuGlnPheLeuLysSerTyrIleThrPheProLeuTyrA 399
Db 1217 AAGTGGGTGGGTGGTGTCTCCAGGTCTCTGACGATACATCCCTCCCGCTAGG 1276
QY 399 lAlaValAlaThrGlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThrAla 419
Db 1277 CGCTGCTCAGCAGATGGGGTGGTGCACATGAAAGAACATCTTCAGAGAGCAGACGGCA 1336
QY 419 sValAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLysValArgAspThr--- 437
Db 1337 AGCGGTGATGTAAGTGGCGCAAGCGCCAAAGCATTAAGNNNNNNNNNNNNNNNN 1396
QY 438 -----AspMetLeuMetAlaGlnMetIleGlyLysAlaThrProSerArgLys 455
Db 1397 NNNNCTCGACGCTGACGAGC-----GCGACACACAGCGGACGACACCGCGG 1447
QY 455 erProMetProSerArgAlaSerSerProValHisLeuLeuHisLysGlyMetGlyArgS 475
Db 1448 CGACGTGCGGAGCGGGGCAATCGCGGCTGCACCTGCTCCACAAGTACAGGGGAGGT 1507
QY 475 erAspAspProGlnSerAlaProThrSerProArgThrMetGluAlaArgAspMet 495
Db 1508 CGAGGACCCGACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCATG 1561
QY 495 yrProValValValAlaHisProValHisArgLeuAsnProAlaAspArgArgTrpSerV 515
Db 1562 ACCCGGTGGCTGACCATGATCGCTGCACAGGTGACACCC---GAGAGGTAGAGCCCG 1618
QY 515 alSerSerSerAlaLeuAspAlaAspIleProSerAlaAspPheSerPheSer 532
Db 1619 CTTGTTCACGCGCGTCAACATGACATTCGCTGATGCGANNNNNNCTTTTACG 1671

RESULT 2
AY108340 1799 bp mRNA linear HTC 25-MAY-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. 1799
/organism="Zea mays"
/db_xref="MaizeDB:637144"
/db_xref="taxon:4577"
/clone="PC0122701"
/clone_id="Maize Mapping Project/DuPont Cornsensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACS in conjunction with the Maize
Mapping Project"

BASE COUNT 378 a 551 c 502 g 368 t
ORIGIN

Alignment Scores:
Pred. No.: 3,35e-120 Length: 1799
Score: 1201.00 Matches: 241
Percent Similarity: 63.29% Conservative: 78
Best Local Similarity: 47.828 Mismatches: 123
Query Match: 43.148 Indels: 62
DB: 11 Gaps: 5

US-09-857-896a-32 (1-534) x AY108340 (1-1799)

QY 10 AAlaAgThleuProGluThrProSerThrPalaValAlaLeuValPheAlaValMetIle 29
DB 73 TCGCGGAGCTTGACACACCGACATGGCGGCGCTCGGTGGCGGCGTATGCTG 132
QY 30 TleValSerValLeuLeuGluNHsAlaLeuHsLysLeuGluHsTrpPheHsLysArg 49
DB 133 CTCATCTCCATCTCTCTGGAGAAAGGCTCCACACAGTGGGAGGATCTCTCCACCGC 192
QY 50 HsLysAsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuIleGly 69
DB 193 AAGAAAGAGCGCATGCTGGAGCGCCCTGGAAAGGTGAAGCGGAGCTCATGGTGGG 252
QY 70 PheIleSerLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGlu 89
DB 253 TTCATCTCTCTCTCTCTGGTTCGCGAGAACTACATCATCAGGTCTGATCAGCAAC 312
QY 90 LysAlaAlaSerIleMetArgProCysSerLeuPro----- 101
DB 313 CAGCGCGGCAACACATGCTCCCTGTGAAGCTCAGAGCGCGCGCTCAGAGGCAAGAC 372
QY 101 ----- 101

DB 373 GGCACAGGCAAGAGAGCGCCCGCTGCTGCTGCCAAGAAAGATCGCCGCTCCGCTC 432
QY 102 ProGlySerValLysSerLysTyr----- 109
DB 433 CCGTGAAGAAAGAAAGAGAGCGCCCGCCCGCCGACATCTTGGCGGTGTGTGAC 492
QY 110 -----LysAspTyrTyrCys----- 114
DB 493 TGGCGCGCGCCCTCTACAGCGGCACAAAGCCAGAGATGCTGGCGAGCGAGATCGCGACC 552
QY 115 ---AlaLysLysGlyLysValSerLeuMetSerThrGlySerLeuHsGluLeuHsIle 133
DB 553 AAGTCCCGCGAGGAGAAAGTGGCGCTCATCTCATCAACAGCCCTGCACAGCTGCACATC 612
QY 134 PheIlePheValAlaValAlaPheHsValThrTyrSerValIleIleMetAlaLeuSer 153
DB 613 TTCATCTCTCTCTCTCGCGCTCTCCAGCTCTCTACAGCGCATACCATGCGCTCGCG 672
QY 154 ArgLeuLysMetArgThrTrpLysLysTrpGluThrGlnAlaSerLeuGluTrpGln 173
DB 673 AGGGCCAAAGATACCTGATGAGAAAGTGGAGAAAGCTGCAGGACAAAGACTACGAG 732
QY 174 PheAlaAsnAspProAlaArgPheArgPheThrHsGlnThrSerPheValLysArgHs 193
DB 733 TTCATCATGATGACCGAGCGGCTTCAGAGTTCCACCGAGACTTCTCTTGTGAGGACGAT 792
QY 194 LeuGly---LeuSerSerThrProGlyIleArgTyrValAlaPhePheArgGlnPhe 212
DB 793 ATGAATGTGCGAAGCAAGTTCCAGCATCATCTTCATCAGCAACTCTTCGCGAGTTC 852
QY 213 PheArgSerValThrLysValAspTyrLeuThrLeuArgAlaGlyPheIleAsnAlaHs 232
DB 853 TTCAGTCCCGAGAGCAGGACGAGCATCTCTCGCGCTCGCGCCACAGCTTGTGCACGCTTC 912
QY 233 LeuSerHsAsnSerLysPheAspPheHsLysTyrIleLysArgSerMetGluAsp 252
DB 913 CTGGCCCTTGCGACCAAGTTGATTCAGAAATGATCATCAAGCGGCTCTCGGAGATGAC 972
QY 253 PheLysValAlaValAlaGlyIleSerLeuProLeuTrpCysValAlaIleLeuThrLeuPhe 272
DB 973 TTCAGGTGATCGTGGGAGATCACTCTCTCTGCTGCGCTTCTCTCATCTCTCTTC 1032
QY 273 LeuAspIleAspGlyIleGlyThrLeuThrTrpIleSerPheIleProLeuValIleLeu 292
DB 1033 CTCACAGCTCATGATGAGCAGACACAGCTCTGGATCTTCATCATGCGGTGTGATCATC 1092
QY 293 LeuCysValGlyThrLysLeuGluMetIleIleMetGluMetAlaLeuGluTrpGlnAsp 312
DB 1093 CTGTGGTGGGAGGAGAAAGTGCAGGAGCATCATCTCCGCAATGCGCATTCACATCAGGAG 1152
QY 313 ArgAlaSerValIleLysGlyLysProValValGluProSerAsnLysPhePheTrpPhe 332
DB 1153 GCGCACGCGCTCATCAGGCGCATCCGATGATGCAATGCAATGCACTCTCTCTCTGCTTC 1212
QY 333 HsArgProAspTrpValLeuPhePheIleHsLysLeuThrLeuPheGlnAsnAlaPheGln 352
DB 1213 GCAGCGCCCACTCTGCGCTCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1272
QY 353 MetAlaHsPheValThrPheValAlaThrProGlyLeuLysLysCysPheHsMetHs 372
DB 1273 ATCATCTACTCTCTCTGATGATCTGTAGTAGTAGGATGAGTCTGCTTCAACACTCC 1332
QY 373 IleGlyLeuSerIleMetLysValIleGluLeuAlaLeuGluIlePheLeuCysSerTyr 392
DB 1333 GAAAGATTGCTCTTGCACAGACTCTGCTGAGCTGTGTTCCAGTGTGTCGAGCTAC 1392
QY 393 IleThrPheProIleuThrAlaValAlaPheIleMetGlySerAsnMetLysArgSerIle 412
DB 1393 GTGAGCTCCCGCTGTACGCGCTGTCTCCAAATGGGCTCCACCATGAAGAGTCTCATC 1452
QY 413 PheAspGluGlnThrAlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLys 432
DB 1453 TTCGACAGAGAGACTCCAAAGGCTCAAGAACTGGCGCGCGCGCCCAAGAAAGAGGCT 1512

QY 433 LysValAlaArgSphrAspMetLeuMetIleGlyAspAlaThrProSerArg 452
Db 1513 CCCACCGCGGC-----TCCAGCAGCGCGGTGGTCCGCCACCGCC 1557
QY 453 GlyThrSerPro 456
Db 1558 GCGGCGAGCCCC 1569

RESULT 3
AY105309
LOCUS AY105309 2013 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PCO148749 mRNA sequence.
ACCESSION AY105309
VERSION AY105309.1 GI:21208387
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 2013)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
TITLE Unpublished (2002)
2 (bases 1 to 2013)
Coe,E.C.
REFERENCE Direct Submission
AUTHORS Submitted (25-APR-2002) Maize Mapping Project, University of
JOURNAL Missouri, Columbia, MO 65211, USA
FEATURES
source
1. 2013
/organism="Zea mays"
/db_xref="taxon:638783"
/db_xref="taxon:4577"
/clone="PCO148749"
/clone_lib="Maize Mapping Project/Dupont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

BASE COUNT 483 a 513 c 516 g 501 t
ORIGIN

Alignment Scores:
Pred. No.: 1,79e-119 Length: 2013
Score: 1195.00 Matches: 262
Percent Similarity: 60.948 Conservative: 75
Best Local Similarity: 47.388 Mismatches: 179
Query Match: 42.928 Indels: 39
DB: 11 Gaps: 6

US-09-857-896A-32 (1-534) x AY105309 (1-2013)

QY 11 ArgThrLeuProGluThrProSerTrpAlaValAlaLeuValPheAlaValMetIleLe 30
Db 147 AGGGGCGGTGAGACAGCGCGACGTGGCGCGCGCGTCTGCTGTCATCGTCGGG 206
QY 31 ValSerValLeuLeuGluHisAlaLeuHisLysLeuGluHisTrpPheHisLysArgHis 50
Db 207 GCGTCATATCTCTCTCGAGGGCTTCTCCACACCTCGGTCAGTTGCTCAACAAGAGCGG 266
QY 51 LysAsnAlaLeuAlaGluAlaLeuGluLysIleLysAlaGluLeuMetLeuValGlyPhe 70
Db 267 AAGAGAGGCGCTGTTGACGCTCTGGAAGGTTAAATGGAGCGATCGAGACTCGGGGTTCC 326
QY 71 IleSerLeuLeuLeuAlaValThrGlnAspProIleSerGlyIleCysIleSerGluLys 90

Db 327 ATATCGTCTGCTGACGCGTACGGAAGGTACATCGCGGCATCTGCATCCCGAGGGA 386
QY 91 AlaAlaSerIleMetArgProCysSerLeuProGlySerValLysSerLysTyrLys 110
Db 387 GCCGCAACACCATCTGCGCTCGCGCTGTCTCCGGTCACTGGTGGGGAAGGCCAAG 446
QY 111 AspTyr-----TyrCysAlaLysLysGly 118
Db 447 GCGCATGCGCGCAGCGCATATGTCAGAGATCCACCAACCATTTTTCCTCGCCCAAGGC 506
QY 119 LysValSerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeu 138
Db 507 ATGTGTGCGCTGTGTTTACGCGAGCGAGCATGCTGCGATTTTCGTGTTCTTCTTG 566
QY 139 AlaValPheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArg 158
Db 567 GCGGTCTTCATGTTACCTTCAGTTCTTCACAAATGTCCTGGTGGTAAGCAAGACTCGT 626
QY 159 ThrTrpLysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAspPro 178
Db 627 ATATGGAAGGTGTGGAAAGAAAGAAACTGTGTCCTCCCTCAGTAAATTTTAATGACCC 686
QY 179 AlaArgPheArgPheThrHisGlnThrSerPheValLysArgHisLeuGlyLysSerSer 198
Db 687 TCAAAAGTCAAGGCTTACGCAACCAACATCTTTGTGAGCAACATGCAAGTTGTGAGAC 746
QY 199 ThrProGlyLysArg---TrpValValAlaPhePheArgGlnPhePheArgSerValThr 217
Db 747 AAAGCAACAATCACGCTGATTTTGAGCTTTTAAAGCAGTTCTTCAGATCGATCCGT 806
QY 218 LysValAspTyrLeuThrLeuAlaGlyPheIleAsnAlaHisLeuSerHisAsnSer 237
Db 807 AAACAGCACTACTTACTTTCGCAATGATGATTTTACGTCATTTATTCGCGGAGACT 866
QY 238 LysPheAspPheHisLysTyrIleLysArgSerMetGluAspAspPheLysValValAl 257
Db 867 AGGTCAATTTTCGAAGTACATTAAGAGGCTCTTGAGAGATGATTCAGACAGCTGTTC 926
QY 258 GlyIleSerLeuProLeuTrpCysValAlaIleLeuThrLeuPheLeuAspIleAspGly 277
Db 927 GGCATTAGTCCACACTAATGGGCTTGTGCTGCTGATCGCTTCCTTCATGTCATGCA 986
QY 278 IleGlyThrLeuThrTrpIleSerPheIleProLeuValIleLeuLeuCysValGlyThr 297
Db 987 TGGCACAACCTTATCTGGTCTCTGCAATTCCTGTTGATTCATCTGAGCTGGAGACA 1046
QY 298 LysLeuGluMetIleIleMetGluMetAlaLeuGluIleGlnAspArgAlaSerValIle 317
Db 1047 AAGCTCGAGGCTATTAATGCTATGATGCTATTGAATATGCCAGAGGCAATACGTTATC 1106
QY 318 LysGlyAlaProValValGluProSerAsnLysPhePheTrpPheHisLysArgProAspTrp 337
Db 1107 CAAGGCAATCGCGGTGTAAACTGAAGTATGATCATTTCTGTGTCGGCAACCTCGTTGG 1166
QY 338 ValLeuPhePheIleHisLysLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHisPheVal 357
Db 1167 GTTCTCCACCTATTCATTTTGGCATCTTCATTCACAAAGCACTTGGAAATTAACATTTCTTT 1226
QY 358 TrpThrValAlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeuSerIle 377
Db 1227 TGGATGTGTAGCAAAATTTGGCTGAGGTCCTGTTCTCCATGACAACTTTGAGTTTATCAT 1286
QY 378 MetLysValValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrIleThrPheProLeu 397
Db 1287 GCAGAGATGTGCTTGGGGCTATGCTGCATTTATTTGACAGTCAATATCACCCCTTCCACTC 1346
QY 398 TyrAlaLeuValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThr 417
Db 1347 TATGCCCTTGTGTTTCAATGATGCTTCAAGATATCAACGAACATTTTTCAGACCAACACA 1406
QY 418 AlaLysAlaLeuThrAsnTrpArgAsnThrAlaLysGlnLysLysValValArgAspThr 437
Db 1407 GCGAAGGCTCTGAAGAAATGGCACAAGCGCGTGTGTGAAGAAACACCAACAGATTCCTC 1466

Qy 438 AspmelluMetalagImellGlyAspalaThproSerArglyThSerPromet 457
Db 1467 TCACACATTCCTCCGAG-----ACTCTAGACATGACACACAGACCT 1511
Qy 458 ProSerArglySerSer-----ProValHisLeuHisLys 470
Db 1512 GCAGGGGAGCGGTGAGTGGCAGCGCTGCAGAGAGTCCGGCTCCGGCAGCTCCACCG 1571
Qy 471 -----GlyMetGlyArgSerAspProGlnSerAlaPro----- 482
Db 1572 TACAGACCATGGCGCAGCTGGCGCGGTAGAGACCCCTTCGACCCGAGCTACAGC 1631
Qy 483 -----ThSerProArgThMetGlnGluAlaArgAspMetTyProValVal 498
Db 1632 GACACGAGCAGCACCGACCGCTGCTGCTGACAGCTAGCAGCTATACCGCGCGCA- 1690
Qy 499 ValAlaHisProValHisArgLeuAspProAlaAspArgArgSerValSerSer 518
Db 1691 GCAGCGGAGCTTCGACACCGAGCGCGGAGGTGCGGTAAGCTC--GTAAGACAGCG 1748
Qy 519 AlaLeuAspAlaAspIleProSerAlaAspPheSerPhe 531
Db 1749 GCGGCGCAGACGACGCTCTCCAGACAGCTCTCGTTC 1787
RESULT 4
BE519781 700 bp mRNA linear EST 23-OCT-2001
LOCUS HV_CEB0021D05f Hordeum vulgare seedling green leaf EST library
DEFINITION HV_CEB0021D05f (Blumeria challenged) Hordeum vulgare cDNA clone
ACCESSION BE519781
VERSION BE519781.2 GI:13266203
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.
REFERENCE 1 (bases 1 to 700)
AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi,
D.W., Fenton, R.D., Oates, R., and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mia6) seedling
leaf cDNA library
Unpublished (2001)
JOURNAL On Aug 8, 2000 this sequence version replaced gi:9743969.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 586
Seq primer: AATTAACTCTCACTAAAGCG
High quality sequence start: 4
High quality sequence stop: 664.
Location/Qualifiers
1..700
/organism="Hordeum vulgare"
/cultivar="C116151 (Mia6)"
/db_xref="taxon:4513"
/clone="HV_CEB0021D05f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HV_CEB0021D05f (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP. Site 1: EcoRI. Site 2: XhoI.
C.I. 16151 (Mia6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA, 7 day old
green seedlings were challenged with isolate 5874 (AYM1a6

) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the T1 Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
plu were in vivo excised to give pBluescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute and picked
Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close T1, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30
(http://webst.pw.usda.gov/gpages/bgn/31/cover.html)."
BASE COUNT 149 a 210 c 191 g 150 t
ORIGIN
Alignment Scores:
Pred. No.: 9,43e-105 Length: 700
Score: 1054.50 Matches: 208
Percent Similarity: 91.91% Conservative: 8
Best Local Similarity: 88.51% Mismatches: 16
Query Match: 37.88% Indels: 3
DB: 10 Gaps: 2
US-09-857-896a-32 (1-534) x BE519781 (1-700)
Qy 94 IlemetArpProCysSerIeu---ProProGlySerValIysSerIyStrIyAspTyR 112
Db 1 GTCATGTGGCCCTGCAAGCGCGGACCGGACCGGACCGCAAGCAAGTACGTGACATAC 60
Qy 113 TTYCysAlaLysIySGIyValSerIeuWetSerhrlYserIeuHisIeuHis 132
Db 61 -----TCCCGAGGGCAGGAGGGCGCTCATGTCCAGCGGACGTTCAGCAGTGGAC 114
Qy 133 IlPheIllePheValLeuAlaValPheHisValThrTySerValIlleIleMetaLeu 152
Db 115 GTCTTCATCTTCGCTCGCGGTCTTCATGACCTACAGCTGATACCATACCTCTTA 174
Qy 153 SerArGlyeulysWetArGThrTrpIyStrIyTrpGlnhrlYhrlAlaSerIeuLuyr 172
Db 175 ACCGCTCTCAAAATGAAACATGAAAGAAATGGAGACAGACACCTCTTGGAAATAC 234
Qy 173 GlnPheAlaAsnAspProAlaArgPheArgPheThrlHisGlnThrSerPheValIyAsr 192
Db 235 CAGTTCACCAATGATCTGCTCAGCGTTCGCGTTCACGACACGACGCTTCGTAAGCGC 294
Qy 193 HisIeuGlyIeuSerSerThrProGlyIleArgTrpValAlaIlePhehArgGlnPhe 212
Db 225 CACCTGGCGCTCTCCAGACACCCCTGCAATCAGATGGGTGGCTCTTTCAGGAGTTC 354
Qy 213 PheArgSerValThrIyValAspTyrIeuThrIeuArgAlaGlyPheIlleAsnAlHis 232
Db 355 TTTCAGGTCACTACCAAGGTGACATCTGACCTTGGGCGCAGCTTCATCAACCGCAT 414
Qy 233 LeuSerHisAsnSerIySAspPheHisIyStrIleIyAsrSerIeuLuyAsp 252
Db 415 TTTCGCAAAACAGCAAGTTCACATTCACAAAGTACATCAAGAGTGCATGAGAGACAC 474
Qy 253 PheIyStrValIyValIyIleSerIeuProIeuTrpCysValAlaIleIeuThrlleuPhe 272
Db 475 TTCAAGGTCTGTGCGCATACGCTCCGCTGTGGGTGTGGCATCTCACCCTCTTC 534

OY 273 Leuaspilaeapgllyleaglythrhleuthrtrpilesesrphelileproleuvalilleu 292
 |||||||.....
 DB 535 CTGCATCATATGAGGGGTGGACGCTCATCTGGATTTCTTCAATCCCTCTGTCATCTC 594.
 OY 293 Leucysvalglythrylsleuglumeillellewecglumetalaleugluillecinsp 312
 |||||||.....
 DB 595 TTGTGTGTGGAAACCAAGCTGAGATGATCATGTGAGATGGCCCTGGAGATCCAGAC 654
 OY 313 ArgAlaserValilleysglvalaprovalvalgluproserasn 327
 |||||||.....
 DB 655 CGGGCAGCCTCATCAAGGGGGCCCCCTGTGTCAGCCAGCAAC 699

RESULT 5
 LOCUS BU484211/c 637 bp mRNA linear EST 23-MAY-2002
 DEFINITION BU484211 K. Sato unpublished cDNA library, strain H602 adult,
 heading stage top three leaves Hordeum vulgare subsp. spontaneum
 cDNA clone bah49h19 3', mRNA sequence.

ACCESSION BU484211 GI:21162659
 VERSION BU484211.1 GI:21162659
 KEYWORDS EST.
 ORGANISM Hordeum vulgare subsp. spontaneum.
 SOURCE Hordeum vulgare subsp. spontaneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 637)

REFERENCE Sato, K., Saisho, D. and Takeda, K.
 AUTHORS Barley EST sequencing project in NIG and Okayama Univ
 TITLE Unpublished (2002)
 JOURNAL Contact: Tadasu Shin-1
 COMMENT Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES
 source
 1. 637
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602"
 /db_xref="taxon:77009"
 /clone="bah49h19"
 /clone_lib="K. Sato unpublished cDNA library, strain H602
 adult, heading stage top three leaves"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 BASE COUNT 119 a 178 c 190 g 150 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2,37e-94 Length: 637
 Score: 959.00 Matches: 182
 Percent Similarity: 96.92% Conservat: 7
 Best Local Similarity: 93.33% Mismatches: 6
 Query Match: 34,45% Indels: 0
 DB: 13 Gaps: 0

US-09-857-896a-32 (1-534) x BU484211 (1-637)

OY 340 Phelpellehlsleuthrleupheglnaenalahepneimetalahispevaltrprhr 359
 |||||||.....
 DB 636 TTCTTCATACACCTGACGTTGTTCCAGAACGGTTTTCAGATGGCGCATTTTGTGTGACA 577
 OY 360 ValAlatrhrProgllyleuylsycyspnehisethisileglyleuserlilemetyls 379
 |||||||.....
 DB 576 GTGGCCAGCCCGGCTTGAAGAAATGCTACACAGCAGATCGGCTGACATCATGAAG 517
 OY 380 ValValleuglyleualaleuglnpheuucyserryrlyrlethrphreproleuvala 399
 |||||||.....
 DB 516 GTGCTGTGGGGCTAGCTCTCCAGCTTCTCTGACACTATAGACCTTCCCGCTTACGGG 457
 OY 400 LeuValthrGlnMetGlySerAsnMetLysArgSerLilepheaspGluInhrAlaLys 419

DB 456 CTGCTACACAGATGGGATCAACATGAGAGGTCATCTTCGACGAGACGAGCTCAAG 397
 |||||||.....
 OY 420 AlaleuthrAsnTTPATgaSnThrAlaLysGluLysLysValArGaSPThrAspMet 439
 |||||||.....
 DB 396 GGGCTACCAATGGCGGAAACGGCCAGAGAAAGAAAGATCCAGACAGGACATG 337
 OY 440 LeuMetAlaGlnMetilegilyaapalatrhrproserargglythrSerPrometProser 459
 |||||||.....
 DB 336 CTGATGGCTCAGATATGCGGCGAGCAACAGCAGACCGATCGTCCGATGCCAGAC 277
 OY 460 ArgAlaserSerProvalHisleuHlsLysGlyMetGlyArgSerAspAPProglin 479
 |||||||.....
 DB 276 CGGGGCTATCACCGCTGACACTGCTTCCACAGAGCATGGGGCTGGACAGACCCGAG 217
 OY 480 SerAlaProThrSerProATgThrMetGluAlaArGaSPMetYrProValAlaVal 499
 |||||||.....
 DB 216 AGCGCCGCCACCTCCCAAGACCCAGCAGAGCGCTAGGACATGTACCGGTTGTGTG 157
 OY 500 AlaHisProValHisArgLeuAsnProAlaAspArgArGaSerValSerSerAla 519
 |||||||.....
 DB 156 GCGCACCGGCTCACAGACTAAATCCATACAGACAGAGAGTCCGCTCATCATCGGC 97
 OY 520 LeuaspAlaaspilileproserAlaaspPneSerPneSerGlnGly 534
 |||||||.....
 DB 96 CTCGAAGCCGACATCCCGAGTGAGATTTTCTTCAGCAGGGA 52

RESULT 6
 LOCUS AV945501/c 669 bp mRNA linear EST 18-JAN-2002
 DEFINITION AV945501 K. Sato unpublished cDNA library, strain H602 adult,
 heading stage top three leaves Hordeum vulgare subsp. spontaneum
 cDNA clone bah26013 3', mRNA sequence.

ACCESSION AV945501 GI:18241298
 VERSION AV945501.1 GI:18241298
 KEYWORDS EST.
 ORGANISM Hordeum vulgare subsp. spontaneum.
 SOURCE Hordeum vulgare subsp. spontaneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 669)

REFERENCE Sato, K., Saisho, D. and Takeda, K.
 AUTHORS Barley EST sequencing project in NIG and Okayama Univ
 TITLE Unpublished (2002)
 JOURNAL Contact: Tadasu Shin-1
 COMMENT Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES
 source
 1. 669
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602"
 /db_xref="taxon:77009"
 /clone="bah26013"
 /clone_lib="K. Sato unpublished cDNA library, strain H602
 adult, heading stage top three leaves"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 BASE COUNT 131 a 182 c 192 g 163 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 2,54e-94 Length: 669
 Score: 959.00 Matches: 182
 Percent Similarity: 96.92% Conservat: 7
 Best Local Similarity: 93.33% Mismatches: 6
 Query Match: 34,45% Indels: 0
 DB: 10 Gaps: 0

US-09-857-896a-32 (1-534) x AY945501 (1-669)

QY 340 PhepheiHsLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHsPheValTrpThr 359
|||||
Db 669 TTCTTCATACACCTGACCTTGTTCACAGACGGCTTTCAGATGCGCCATTTGTGTGACA 610

QY 360 ValAlaThrProGlyLeuAlaLysCysPheHsMetHsIleGlyLeuSerIleMetLys 379
|||||
Db 609 GTGGCCAGCGCCGGCTTGAGAAATGCTACACAGCCAGCATCGGGCTGACATCATGAAAG 550

QY 380 ValValLeuGlyLeuAlaLysGlnPheLeuCysSerTrpIleThrPheProLeuTyraLa 399
|||||
Db 549 GTGGCTGTGGGGCTAGCTCTCCAGTTCTCTGAGCTATAGACCTTCCCTCTCTAGCGG 490

QY 400 LeuValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGlnGlnThrAlaLys 419
|||||
Db 489 CTCGTACACAGATGGATGAACATGAAGAGGTGCTCATCTTCAGACAGACGCTCAAG 430

QY 420 AlaLeuThrAsnTrpArgAsnThrAlaLysGlyLysValArgAspThrAspMet 439
|||||
Db 429 GCGCTCACCACTGGCGGACACGCGCAAGAGAAAGAAAGTCCAGACAGGACATG 370

QY 440 LeuMetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSerPrometProser 459
|||||
Db 369 CTGATGGCTCAGATGATGCGGACGACACGAGCGCGGCTGCGCGATGCCGAGC 310

QY 460 ArgAlaSerSerProValHsLeuHsLysGlyMetGlyArgSerAspAspProGln 479
|||||
Db 309 CGGGCTCATACCCGTGACACTGCTTCACAAAGGATGGGCGGTGCGACGCCCGAG 250

QY 480 SerAlaProThrSerProArgThrMetGlnGlnAlaArgAspMetTrpProValVal 499
|||||
Db 249 AGCGGCGCCACCTCGCAGACGCCAGGAGGAGGCTAGGACATGTACCGCGTGGTG 190

QY 500 AlaHsProValHsArgLeuAsnProAlaAspArgArgSerValSerSerAla 519
|||||
Db 189 GCGCACCGGCTGCACACACTTAATCTTAACGACAGAGAGAGTCCGCTCATATGAGCC 130

QY 520 LeuAspAlaAspIleProSerAlaAspPheSerPheSerGlnGly 534
|||||
Db 129 CTCGAAGCCGACATCCCGATGCGATTTTCTTCACCGAGGA 85

RESULT 7
BJ483019/c 671 bp mRNA linear EST 23-MAY-2002
LOCUS BJ483019 K. Sato unpublished cDNA library, strain H602 adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
ACCESSION BJ483019 GI:21161473
VERSION BJ483019
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 671)
AUTHORS Sato, K., Saisho, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yatai Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 671
/organism="Hordeum vulgare subsp. spontaneum"
/db_xref="taxon:77009"
/clone="Bah2J24"

/clone_11b="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"

BASE COUNT 131 a 181 c 193 g 164 t 2 others

ORIGIN

Alignment Scores:
Pred. No.: 2,55e-94 Length: 671
Score: 959.00 Matches: 182
Percent Similarity: 96.92% Conservative: 7
Best Local Similarity: 93.33% Mismatches: 6
Query Match: 34.45% Indels: 0
DB: 13 Gaps: 0

US-09-857-896a-32 (1-534) x BJ483019 (1-671)

QY 340 PhepheiHsLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHsPheValTrpThr 359
|||||
Db 671 TTCTTCATACACCTGACCTTGTTCACAGACGGCTTTCAGATGCGCCATTTGTGTGACA 612

QY 360 ValAlaThrProGlyLeuAlaLysCysPheHsMetHsIleGlyLeuSerIleMetLys 379
|||||
Db 611 GTGGCCAGCGCCGGCTTGAGAAATGCTACACAGCCAGATCGGGCTGACATCATGAAAG 552

QY 380 ValValLeuGlyLeuAlaLysGlnPheLeuCysSerTrpIleThrPheProLeuTyraLa 399
|||||
Db 551 GTGGCTGTGGGGCTAGCTCTCCAGTTCTCTGAGCTATAGACCTTCCCTCTCTAGCGG 492

QY 400 LeuValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGlnGlnThrAlaLys 419
|||||
Db 491 CTCGTACACAGATGGGATGAACATGAAGAGTTCATCTTCACAGACAGCGTCCAG 432

QY 420 AlaLeuThrAsnTrpArgAsnThrAlaLysGlyLysValArgAspThrAspMet 439
|||||
Db 431 GCGCTCACCACTGGCGGACACGCGCAAGAGAAAGTCCGAGACACGCGACATG 372

QY 440 LeuMetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSerPrometProser 459
|||||
Db 371 CTGATGGCTCAGATGATGCGGACGACACCGAGCGGAGGCTGCGCGATGCCGAGC 312

QY 460 ArgAlaSerSerProValHsLeuHsLysGlyMetGlyArgSerAspAspProGln 479
|||||
Db 311 CGGGCTCATACCCGTGACACTGCTTCACAAAGGATGGGCGGTGCGACACGCCCGAG 252

QY 480 SerAlaProThrSerProArgThrMetGlnGlnAlaArgAspMetTrpProValVal 499
|||||
Db 251 AGCGGCGCCACCTCGCAGACGCCAGAGAGGAGGCTAGGACATGACCGGTTGTGAG 192

QY 500 AlaHsProValHsArgLeuAsnProAlaAspArgArgSerValSerSerAla 519
|||||
Db 191 GCGCACCGGCTGCACACACTTAATCTTAACGACAGAGAGGATCGCGCTCATATGAGCC 132

QY 520 LeuAspAlaAspIleProSerAlaAspPheSerPheSerGlnGly 534
|||||
Db 131 CTCGAAGCCGACATCCCGATGCGATTTTCTTCACCGAGGA 87

RESULT 8
BJ478030 602 bp mRNA linear EST 23-MAY-2002
LOCUS BJ478030
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
ACCESSION BJ478030 GI:21156521
VERSION BJ478030
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 602)
AUTHORS Sato, K., Saisho, D. and Takeda, K.

TITLE	Barley EST sequencing project in NIG and Okayama Univ
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasu Shin-I

BASE COUNT	126 a	174 c	159 g	142 t	1 others
ORIGIN					

US-09-857-896A-32 (1-534) x BJ478030 (1-602)

QY	109	TYLPLAASATYTYTTCYALALALYLSGLYVSLSERLMESERTNGLYSERLU	128
	111		128
DB	3	TAGGTGACTAC-----TGCCGGGNGGCAAGTGGGGCTCATGTCCAGGGGCACTTG	56
QY	129	HISGLNLEHNIISLEPHEILEPHEVALLEUALVALPHEHISVALTHRYTSERVALIE	148
	131		148
DB	57	CACCACCTCAGCTTCATTCATTCGTGCTGGGGCTTCACATGTCACCTCAGCAGCTC	116
QY	149	ILEMERALEUSERARGLEULYSMETARGTHTRPLRYSLSTRPGIUTNGLIUTNRLA	168
	151		168
DB	117	ACCATAGCTCTAAGCCGCTCCAAATAGAACATGGAAGAAATGGAGACAGACCACC	176
QY	169	SETLEUGLUTYGLINPHEALIASASPRIOLATARGPHEATARGPHEITHHISGLNTHRSR	188
DB	177	TCTGTGAATACAGTGTGCAGAAATGATCTGCACGGTGTCCGGTCCAGCACACAGAGCTGG	236
QY	189	PHEVALLYSARGHISLEUGLYLEUSERSERTHTRPGIYILEATGTPVALVALAPHE	208
	191		208
DB	237	TTCGTGAAGCGCACCTGGGGCCTCTCCAGCACCCCTGGCATCAGATGGAGTGGGCTTC	296
QY	209	PHEARGLINPHEPARGSERVALTHRLYSLVALASPTYRLLEUTHRLHEUALARGVALI	228
	211		228
DB	297	TTCGGGAGTCTCTCAGGTCAAGTCCACCAAGTGTGACTCTGACCTTGAGGCCAGGCTTC	356
QY	229	ILEASNALHISLEUSERHISASNSERLYSPHEASPHENHISLYTYRILEYARGSER	248
	231		248
DB	357	ATCACACCGCATTTGTCGCAAAACAGCAAAATGTGACTTCACAAAGTACATCAAGAGGTGG	416
QY	249	METGLIASAPSPHELYSLVALVALVALGLIISERLEUPROLEUTPQYSVALAIAIE	268
	251		268
DB	417	ATGGAGAGACACTCAAGGTGTGTGGGTGGGATCAGGCTCCCGCTGTGGGTGTGGGATC	476
QY	269	LEUTHRLLEUPHELEUASPILEASPGYILEGLYTHRLLEUTHTRIPILIESERPHLEPRO	288
	271		288
DB	477	CTCACCCCTCTTCCTTGACATCAATAGGGGTGGCAGCCGATCATCTGGATTTCTTCATCCCT	536
QY	289	LEUVALILELEULEUCYVALGLYTHRLYSLLEUGLUMETILEIIMETGLIUMETALALU	308
	291		308
DB	537	CTGTGTATCTCTTGTGTGTGGAAACCAACCTGTGAGATGATCATCATGAGATGGCCCTG	596
QY	309	GLUILE 310	

Db 597 GAGATC 602

LOCUS	667 bp	mRNA	linear	EST 23-MAY-2002
DEFINITION	<p>BJ485666 K. Sato unpublished cDNA library, strain H602 adult, heating stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone ban58c07 3', mRNA sequence.</p>			

ACCESSION	BJ485696
VERSION	BJ485696.1
KEYWORDS	GI:21164138
SOURCE	EST.
ORGANISM	Hordeum vulgare subsp. spontaneum
REFERENCE	Hordeum vulgare subsp. spontaneum

REFERENCE 1 (bases 1 to 667)

TITLE	Barley EST sequencing project in NIG and Okayama Univ.
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasu Shin-I

FEATURES	Location/Qualifiers
source	1. .667

BASE COUNT	129 a	181 c	192 g	163 t	2 others
ORIGIN					

US-09-857-896A-32 (1-534) x BJ485696 (1-667)

QY	341	PLIIIEHISLEUTHRIEUPHEGINSNALPHGIMETALAHISPHVALTRIPHRVAL	360
Db	665	TTTATACACCTGACGCTGTTCCAGAACCCGTTTCACATGGCCGCAATTTGTGTGACAGTG	608
QY	361	AlaThrProGlyLeuLeuIstYscYsPheHisIleMetHisIleGlyLeuSerLleMetIstYsAl	380
Db	605	GGCAGCCCGGCTTGAAAGAAATGTCTTACCAACACGCGATGGGGCTGACATCATGAAGGGTG	546
QY	381	ValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrLleThrPheProLeuTyrAlaLeu	400
Db	545	GTGTGGGGCTAGCTCCACAGTTCCTCTGCGAGCTAATATACCTTCCCTTACAGGGCTC	486
QY	401	ValThrGlnMetGlySerAsnMetLysrYsSerLlePheAspGlnGlnThrAlaLysAla	420
Db	485	GTCACACAGATGGGATCAAAACATGAAGAGGTCCATCTTGACAGACGAGCTCAAGGCGG	426
QY	421	LeuThrAsnTyrPAsnThrAlaThrAlaGluIstYsLysValArgAspThrAspMetLeu	440
Db	425	GTACCAACATGGCCGAACACGGCCAGAGAGAAAGAAAGTCCAGACACGACATGCTG	366
QY	441	MetAlaGlnMetLleGlyAspAlaThrProSerArgGlyThrSerProMetProSerArg	460

Accession	Version	Keywords	Source	Organism	Reference	Title	Authors	Journal	Comment
365	ATGCGTCACATGATGGCGGACGCAACCGAGCGAGGCTGTCGCCGATGCCAGCGCG								
461	AlaSerSerProValHisLeuLeuHisIstysgIywtglYarSerAspAspProGlnSer								
305	GCGTCATCAACCGGTCACCTGCTTTCACAAAGGACATGAGGCGGTCGACACACCCCAAGC								
481	AlaProThrSerProArgThrMetGlnGlnAlaIarTgAspMetTyrProValValAla								
501	HisProValHisArgLeuAsnProAlaAspArgArgSerValSerSerSerAlaLeu								
185	CACCGGTCACAGCTCAATCTTAACGACAGAGGAGGAGTCCGCCATCAATGAGGCTC								
521	AspAlaAspIleProSerAlaAspPheSerPheSerGlnGly								
125	GAAGCCGACATCCCAAGTCAGATGCAATTTTCTTCAGCCAGCGGA								
668	TTCAATACACCTGAGAGTGTTCCAGAAACCGTTTCAGATGAGCGCATTTTGTGTGACAGTG								
361	AlaThrProGlyLeuLeuIstysgCysPheHisMetHisIstGlyLeuSerIleMetIysVal								
608	GCGACGCGCGGCTTGAAAGAAATGCTTACCAACACAGAGATCGAGGCTAGCATCATGAAGTG								
461	AlaSerSerProValHisLeuLeuHisIstysgIywtglYarSerAspAspProGlnSer								
305	GCGTCATCAACCGGTCACCTGCTTTCACAAAGGACATGAGGCGGTCGACACACCCCAAGC								
481	AlaProThrSerProArgThrMetGlnGlnAlaIarTgAspMetTyrProValValAla								
501	HisProValHisArgLeuAsnProAlaAspArgArgSerValSerSerSerAlaLeu								
185	CACCGGTCACAGCTCAATCTTAACGACAGAGGAGGAGTCCGCCATCAATGAGGCTC								
521	AspAlaAspIleProSerAlaAspPheSerPheSerGlnGly								
125	GAAGCCGACATCCCAAGTCAGATGCAATTTTCTTCAGCCAGCGGA								
668	TTCAATACACCTGAGAGTGTTCCAGAAACCGTTTCAGATGAGCGCATTTTGTGTGACAGTG								
361	AlaThrProGlyLeuLeuIstysgCysPheHisMetHisIstGlyLeuSerIleMetIysVal								
608	GCGACGCGCGGCTTGAAAGAAATGCTTACCAACACAGAGATCGAGGCTAGCATCATGAAGTG								

[illegible]

Score: 953.00 Matches: 181
 Percent Similarity: 96.91% Conservative: 7
 Best Local Similarity: 93.30% Mismatches: 6
 Query Match: 34.23% Indels: 0
 DB: 13 Gaps: 0

US-09-857-896a-32 (1-534) x BU482842 (1-681)

QY 341 PheilleHstleuthrleupheclinsnAlaheclimetaHstpheValtrphtyal 360
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 DB 661 TTCATACACCTGACGTTGTTCCAGAACCGCTTCAGATGCGCATTTTGTGGACACTG 622
 QY 361 AlAthrProglyleuylsycyspHsthisHstisHleglyleuSerHleMetysVal 380
 |||||||
 DB 621 GCCAGCCCGGCTTGAAAGAAATGTCACACACGAGATCGGCTGAGCATGAAAGGTG 562
 QY 381 ValleuclyleuAlaleuclnPhleucysSerYrHlethrheProleuYrAlaleu 400
 |||||||
 DB 561 GTCTGGGGCTACCTCTCCAGTTCCTGCGCTATATGACCTTCCCTCTACGCGCTC 502
 QY 401 ValThrglnMetglySerAsnMetLysArgSerHlePheaspGluclnThraAlaLysAla 420
 |||||||
 DB 501 GTCACACAGATGGATCAAAATGAAAGAGTCCATCTTCAGACGACAGCTCAAGGCG 442
 QY 421 LeuthrasntrpargsntrhrAlaLysGluLysLysValArgAspHraspHmetleu 440
 |||||||
 DB 441 CTCACACACTGGGGAGAACGGCCAGAGAGAAAGAAAGTCCGACACGACAGATGCTG 382
 QY 441 MetaGlnMetHleGlyAspAlaThrProSerArgLysThrSerPrometProSerArg 460
 |||||||
 DB 381 ATGGCTCAGATGATCGCGCGACCAACCGAGCGAGCTCGCGCGATGCGGAGCGCG 322
 QY 461 AlaSerSerProValHstleuHstleuHstLysGlyMetGlyArgSerAspProGlnSer 480
 |||||||
 DB 321 GGCTATCATCCCTGCACTGCTTCACAAAGGCGATGGGGCGGTGCGACACCCCAAGAC 262
 QY 481 AlaProThrSerProArgThrMetGluAlaArgAspMetYrProValValAla 500
 |||||||
 DB 261 GCGCCACACTGCGCCAGAGACCGAGAGGCTAGGAGCATGTACCGGCTTGTGTGCGC 202
 QY 501 HstProValHstArgleuAsnProAlaAspArgArgSerValSerSerSerAlaleu 520
 |||||||
 DB 201 CACCCGGTGCACAGACTAAATCTTAACGACAGAGAGAGTCCGCTCATCATCGGCCCTC 142
 QY 521 AspAlaAspHleProSerAlaAspHeserPheSerGlnGly 534
 |||||||
 DB 141 GAAGCCGACATCCCACTGCAATTTTCTTCACAGCAGGA 100
 RESULT 12
 BE405266 536 bp mRNA linear EST 21-JUL-2000
 LOCUS WHE1210_E11_I2225 Wheat etiolated seedling root cDNA library
 DEFINITION Triticum aestivum cDNA clone WHE1210_E11_I222, mRNA sequence.
 ACCESSION BE405266
 VERSION BE405266.1 GI:9364734
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae
 ; Triticeae; Triticum.
 1 (bases 1 to 536)
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
 ,P.S., Hsieh,C.C., Kang,Y., Iazo,G.R., Miller,R., Rausch,C.J.,
 Seaton,C.L. and Tong,J.C.
 The structure and function of the expressed portion of the wheat
 genomes
 Unpublished (2000)
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 510559573

Fax: 5105595818
 Email: oanderson@w.ars.ars.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Strategene SK primer.
 Location/Qualifiers

FEATURES

source

1..536
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE1210_E11_I22"
 /clone_1b="Wheat etiolated seedling root cDNA library"
 /tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Seeds were surface-sterilized
 germinated and grown aseptically in the dark at room
 temperature on filter paper with water, nystatin and
 ceftaxime in covered crystallization dishes. Roots were
 harvested. The tissue, total RNA, and poly(A) RNA were
 prepared, a cDNA library was made, and the cDNA clones
 were in vivo excised to give phagescript phagemids in the
 T3 Close lab (Choi, Close, Fenton) at the University of
 California, Riverside. Plasmid DNA preparations and DNA
 sequencing were performed in the Olin Anderson lab (all
 other authors)"

BASE COUNT 117 a 173 c 136 g 110 t
 ORIGIN

Alignment Scores:

Pred. No.: 7.09e-89 Length: 536
 Score: 908.00 Matches: 175
 Percent Similarity: 98.88% Conservative: 2
 Best Local Similarity: 97.77% Mismatches: 1
 Query Match: 32.61% Indels: 1
 DB: 10 Gaps: 0

US-09-857-896a-32 (1-534) x BE405266 (1-536)

QY 69 GlyPheHleSerLeuLeuAlaValThrglnAspProHleSerGlyHleCysHleSer 88
 |||||||
 DB 2 GGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61
 QY 89 GluLysAlaHleSerHleMetArgProCysSerLeuProProGlySerValLysSerLys 108
 |||||||
 DB 62 GAGAGAGCGCCAGCATATCGGCGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
 QY 109 TyrLysAspTyrTyrCysAlaLysLysGlyLysValSerLeuMetSerThrGlySerLeu 128
 |||||||
 DB 122 TACAAAGACTACTACTGCGCCAAACAGGAGCAAGTGTCCCTCATGTCCACGCGAGCTTG 181
 QY 129 HstGlnHstHstHlePheHlePheValLeuAlaValPheHstValThrTyrSerValHle 148
 |||||||
 DB 182 CACCAAGCTGACATATTCATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 QY 149 HleMetAlaLeuSerArgLeuLysMetArgThrTyrLysLysTyrGluThrAla 168
 |||||||
 DB 242 ATCATGGCTCTTAAGCGCTCTCAAAATGAGAACTGGAAAGAAATGGAGACAGAACCGCC 301
 QY 169 SerLeuGluTyrGlnPheAlaAsnAspProAlaArgPheArgPheThrHstGlnThrSer 188
 |||||||
 DB 302 TCCCTGGAATACCACTTGGCAATATGATCTCGCGGCTTCCGCTTACGCCACAGACGTG 361
 QY 189 PheValLysArgHstLysGlyLysSerSerThrProGlyHleArgTyrPval-ValAlaAsp 208
 |||||||
 DB 362 TTCGTGAACGCGCACCTGGGCTCTCCAGACACCCCGGCGTGCAGATGGGTGGTGGCTT 421
 QY 208 ePheArgGlnPhePheArgSerValThrLysValAspTyrLeuThrLeuArgAlaGlyP 228
 |||||||
 DB 422 CTTCAGGCACTTCTTCAGGTGCTGCTACCAAGGTGACATGCTACCTTGAGAGGAGGCTT 481
 QY 228 eHleAsnAlaHstLeuSerHstAsnSerLysPheAspPheHstLysTyrHleLys 246

Db 482 CATCAACGGCAGATTGTGTCATTAACAGAGTTGACCTTCCACAGTACATCAAG 536

RESULT 13

AY104078

LOCUS AY104078 1798 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC0070411 mRNA sequence.
ACCESSION AY104078
VERSION AY104078.1 GI:21207156
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1798)
AUTHORS Halney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitstilt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

TITLE

Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1798)
AUTHORS Coe, E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

FEATURES

source
1..1798
Location/Qualifiers

/organism="Zea mays"
/db_xref="MaizeDB:63833"
/db_xref="taxon:4577"
/clone="PC0070411"
/clone_id="Maize Mapping Project/Dupont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

BASE COUNT 458 a 378 c 490 g 472 t
ORIGIN

Alignment Scores:

Pred. No.: 1 64e-87 Length: 1798
Score: 902.50 Matches: 192
Percent Similarity: 57.80% Conservative: 97
Best Local Similarity: 38.40% Mismatches: 169
Query Match: 32.42% Indels: 42
DB: 11 Gaps: 8

US-09-857-896a-32 (1-534) x AY104078 (1-1798)

OY 1 MetAlaGluAspTyrGluTyrProPheAlaArgThrLeuProGluThrProSerThrAla 20
Db 76 ATGGCGGGCCGAGGGGAG-----GGCGGGCGCGTGAAGTTCACACGACGTGGATC 126
OY 21 ValAlaLeuValPheAlaValMetLeuLeuValSerValLeuLeuGluHisAlaLeuHis 40
Db 127 GTGCGGGCGGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCA 186
OY 41 LysLeuGlyHisLysTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGly 60
Db 187 TACCTGGCAAGACGCTCAGAGAGAAAGAACAGACGCTTTCGAGGCGCTGTCTCAAG 246
OY 61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuLeuAlaValThrGlnAsp 80
Db 247 GTCAAAAGAGAGTTCGATGCTTCTGGGGTTCATCTCCCTGTGACGGTGTTCAGGGG 306
OY 81 ProIleSerGlyIleCysIleSerGlyLysAlaAlaIleSerIleMetArgProCysSerLeu 100
Db 307 ATGATCCGAGAGAGCTGATCCCTGAACGCTGACATTTCACATGCTGTGCAGAGAAAG 366

OY 101 PropGlySerVal---LysSerLysTyrLysAspTyrTyr-----CysAlaLysLysGly 113
Db 367 CCAGATGAGAAAGCGCGGTGAGCCGCCACCATGAGACATTTTGTAGGAGCGCTTGGCAGG 426
OY 114 -----CysAlaLysLysGly 118
Db 427 ATCGGTAGCGCTGTGTCAGAGAAAGCACTGCTGGCGCTGAGCAATTCACGAAGAAAGGA 486
OY 119 LysValSerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeu 138
Db 487 AAGGTCCACTTTGTCCTTGAAGCCATCACTGACGTCACATTTTCATATTGTTCGTG 546
OY 139 AlaValPheHisValThrTyrSerValIleIleMetAlaLeuSerAlaGluLeuLysMetArg 158
Db 547 GCATACACACATGTTATTTCACGCGTCACAACTATGCTTTAGAGAGGTGACAGATACAC 606
OY 159 ThrTrpLysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPheAlaAsnAspPro 178
Db 607 CAATGAAACAGTGGAGAAAT-----GGAATTAAGAAAGATGCTCTCGAATATGCG 657
OY 179 AlaArgPheArgPheThrHisGlnThrSerPheValLysArgHis-----LeuGly 195
Db 658 CCTAAGTAAACCAATGTACATCATCATGATTTATCAAGAAAGCTTTTAAGGTATATGCG 717
OY 196 LeuSerSerThrProGlyIleArgTyrValAlaPhePheArgGlnPhePheArgSer 215
Db 718 AAGATTTCTATATAA---TTGAGTGTGCGCTCTTTTGGTGAAGCGTTTATGATCA 774
OY 216 ValThrLysValAspTyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLysSerHis 235
Db 775 GTATCTAATACATGATACACCAAGCGCTGTGTTTATCATGACTGACTCCCTGGA 834
OY 236 AsnSerLysPheAspPheHisLysTyrIleLysArgSerMetGlnAspPheLysVal 255
Db 835 AATCCAAATTTGATTTCCATGATACATGATGAGGTTTAAAGGGGATTTTAAAGAA 894
OY 256 ValValGlyLeuSerLeuProLeuTyrCysValAlaIleLeuThrLeuPheLeuAspIle 275
Db 895 GTGGTAGCATAAAGCTGTGACTGTGGGTCTCGGAGTGAATTTGTGGTGAATGT 954
OY 276 AspGlyIleGlyThrLeuThrThrPheSerPheLeuProLeuValIleLeuLeuVal 295
Db 955 AATGCTGCGACACATCTTTTGGATGGCTTCTCTCCCTATCTCTCTGTTAGCAAT 1014
OY 296 GlyThrLysLeuGluMetIleIleMetGluMetAlaLeuGluIleGlnAspArgLaser 315
Db 1015 GGCACATAAGCTGAGCATGTCAAGCTCAGTACGCCATGATGAGCTGAGAACACACA 1074
OY 316 ValIleLysGlyAlaProValAlaGluProSerAsnLysPhePheThrPheHisArgPro 335
Db 1075 GCGGTGAGGCGCATGTGATCGTAAACATCAAGTACAGCTTGTGGTGGCAAGGCT 1134
OY 336 AspTyrValLeuPhePheIleHisLeuThrLeuPheGlnAsnAlaPheGlnMetAlaHis 355
Db 1135 AGGGTATACCTTTACCTGATCCATTCCTCTTTAGATGCGTTTGAATTCGTTT 1194
OY 356 PheValIleThrPheValAlaThrProGlyLeuLysLysCysPheHisMetHisIleGlyLeu 375
Db 1199 TTCTTCGTGAGTACAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1254
OY 376 SerIleMetLysValValLeuGlyLeuAlaLeuGlnPheLeuCysSerTyrIleThrPhe 395
Db 1255 ATTTGCCAAGGCTTGTCACTGGGGTGTATTGAGCTTCTGACGATACAGCACTTGG 1314
OY 396 ProLeuTyrAlaLeuValThrGlnMetGlySerAsnMetLysArgSerIlePheAspGlu 415
Db 1315 CCGTGTATGCAATTTGTAACCCAGATGGGAGCGTGTCAAGAAAGAGATCTTCAACAG 1374
OY 416 GlnThrAlaLysAlaLeuThrAsnTyrArgAsnThrAlaLysGluLysLysValAr 435
Db 1375 CATGTGACGAGAGCGCTGTGGGCTGTGAGAGTCAAGTGAAGAAAGGAGCATGAG 1434
OY 435 GAspThrAspMetLeuMetAlaGlnMetIleGlyAspAlaThrProSerArgGlyThrSe 455

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Db 1435 GGAGCTGCATCTGCTA-----GCAAGACGAAATCGA-----TT 1467
Qy 455 rPromePrOserArghAlaSerSerProValHisLeuLeuHisGlyMetGlyArg 474
Db 1468 ACCAATGCCGATTCGCGACGACCTTCCTTAAGATGTAAATGCGAAGCGTGGAGG 1525
RESULT 14
LOCUS B1287602/c 610 bp mRNA linear EST 09-APR-2002
DEFINITION B1287602 y. Ogihara unpublished cDNA library, wh_r Triticum
aestivum cDNA clone wh20n2 3', mRNA sequence.
ACCESSION B1287602
VERSION B1287602.1 GI:20106578
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
1 (bases 1 to 610)
REFERENCE
AUTHORS Ogihara,Y. and Mural,K.
TITLE Expressed genes in Triticum aestivum
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
LOCATION/Qualifiers
FEATURES
source
1. 610
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/cultivar="Chinese Spring"
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/tissue_type="root"
/dev_stage="Feekes' scale 1"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site.1: EcoRI; Site.2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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BASE COUNT 120 a 172 c 173 g 144 t 1 others

ORIGIN

Alignment Scores:

Pred. No.:	8e-87	Length:	610
Score:	890.00	Matches:	172
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	31.97%	Indels:	0
DB:	13	Gaps:	0

US-09-857-896A-32 (1-534) x B1287602 (1-610)

Qy 363 PROGLYLEUtlYsCysPheHISMetHISIEGLYLEuSerIIEMetLysValIleu 382

Db 603 CGGGGCTTGGAAGAAATGCTTCATATGCAATCGGCTCGACATCATGAAGCGCGCG 544

Qy 383 GLYLEUAlaleuGlnPheLeuCySsetYrIIEtrPheProLeuTYrAlaleuValItr 402

Db 543 GGGCTGGCTTCAGATTCTCTGACATATACCTTCCCTTACGGCGCTGCACA 484

Qy 403 GlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThrAlaLysAlaLeuThr 422

Db 483 CAAATGGGATCGAACAATGAGAGGTCCATTTTCAGACGACGACGCGCAAGCGCGTACC 424

Qy 423 AsnTPArgAsnThrAlaLysGluLysValAlaArgPThrAspMetLeuMetAla 442

Db 423 AACTGGCGAACAACGCCAAGAGAAAGAAAGAGTCCGAGACACGACATGCTGATGGCG 364

Qy 443 GlnMetIIEGLYAspAlaThrProSerArgGlyThrSerProMetProSerArgAlaSer 462

Db 363 CAATATATCGCGGACGACGACGCCACGACGACGACATCCCATGCCAGCGGGCTGCG 304

Qy 463 SerProValHisLeuLeuHisLysGlyMetGlyArgSerAspAspProGlnInsertAlaPro 482

Db 303 TCACCGGTACCTGCTTCACAAAGGCGATGGAGCGGTCCGAGATCCCAAGAGCGCGCG 244

Qy 483 ThrSerProArgThrMetGlyGluAlaArgAspMetTyProValValAlaIleAspPro 502

Db 243 ACCTCCGCAAGACCATGAGAGAGGATGAGGATATGACCGGCTGTGGTGGCATGCC 184

Qy 503 ValHisArgLeuAsnProAlaAspArgArgArgSerValSerSerSerAlaLeuAspAla 522

Db 183 GTGACAGACTAAATCTGCTGACAGCGGAGGTGCTCTTCGTGGCACCTGATGCC 124

Qy 523 AspIleProSerAlaAspPheSerPheSerGlnGly 534

Db 123 GACATCCCGACGCGCAGATTTTCTTCAGCGACGAGA 88

RESULT 15

LOCUS B0752866 689 bp mRNA linear EST 23-JUL-2002

DEFINITION WHE4120_A08_B16S Wheat salt-stressed root cDNA library Triticum

ACCESSION B0752866

VERSION B0752866

KEYWORDS B0752866.1 GI:21930648

SOURCE EST.

ORGANISM bread wheat.

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

; Triticaceae; Triticum.

1 (bases 1 to 689)

REFERENCE

AUTHORS Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., Deal,K., Dvorak,J.,

Lazo,G.R., Pham,J., Rausch,J., Wilson,C. and Woo,J.

TITLE The structure and function of the expressed portion of the wheat

genomes - Salt-stressed root cDNA library

JOURNAL Unpublished (2002)

COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@wp.usda.gov

Sequences have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: SK primer.

LOCATION/Qualifiers

1. 689

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE4120_A08_B16"

/clone_lib="Wheat salt-stressed root cDNA library"

/tissue_type="Roots"

/dev_stage="Full tillering"

/lab_host="E. coli SOLR"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid

pluescript SK(-): Site.1: EcoRI; Site.2: XhoI; Hydroponic

plants grown to full tillering stage were treated with 150

mM NaCl for either 12 hours or 7 days. Root tissues of the

plants subjected to both types of treatment were collected

separately at University of California, Davis (E. Akhunov and K. Deal in J. Dvorak's Lab). Total RNA was prepared separately from the two samples (12h and 7day treatments), and equal amount of RNA was then pooled. PolyA RNA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pluescript SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak) at the University of California, Davis. Colony plating, plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 139 a 221 c 200 g 129 t
ORIGIN

Alignment Scores:

Pred. No.:	1 97e-85	Length:	689
Score:	878.00	Matches:	170
Percent Similarity:	98.85%	Conservative:	2
Best Local Similarity:	97.70%	Mismatches:	0
Query Match:	31.54%	Indels:	0
DB:	14	Gaps:	0

US-09-857-896A-32 (1-534) x BQ752866 (1-689)

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Oy      1 MetLagLusPyrGluTyrProAlaArgThrLeuProGluThrProSerTrpAla 20
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Db      166 ATGGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 225

Oy      21 ValAlaLeuValPheAlaValMetIleValSerValLeuLeuGluHisAlaLeuHis 40
         |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
Db      226 GTGGCCCTGCTGTGCGCGTATGATCATCGTCTGCTCTCTGAGCAGCGCTCCAT 285

Oy      41 LysLeuGlyHisTrpPheHisLysArgHisLysAsnAlaLeuAlaGluAlaLeuGluLys 60
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Db      286 AAGCTGGCCATTGGTTCACAAAGGCGACAAAGACCGCTGCGAGGCGCTGGAGAG 345

Oy      61 IleLysAlaGluLeuMetLeuValGlyPheIleSerLeuLeuAlaValThrGlnAsp 80
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Db      346 ATCAAGGCGGAGCTATGCTGGTGGCTTATCTCCGCTGCTGCGCTGACGACAG 405

Oy      81 ProIleSerGlyTleCysIleSerGluLysAlaIleSerIleMetArgProCysSerLeu 100
         |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
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Oy      101 ProProGlySerValLysSerLysTyrLysAspTyrTyrCysAlaLysLysGlyLysVal 120
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Db      466 CCCCTGGCTCCGTCAGAGCAAGTACAAAGACTACTGGGCCCAAGAGGCAAGGTG 525

Oy      121 SerLeuMetSerThrGlySerLeuHisGlnLeuHisIlePheIlePheValLeuAlaVal 140
         |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
Db      526 TCGCTCATGTCCAGCGGAGCTGTGCACCACTGCACATATTCATCTTGTGTCGCCGTC 585

Oy      141 PheHisValThrTyrSerValIleIleMetAlaLeuSerArgLeuLysMetArgThrTrp 160
         |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
Db      586 TTCATGTACCTACACAGCATCATGCTTAAGCCGTCCTCAAAATAGAGAACTGG 645

Oy      161 LysLysTrpGluThrGluThrAlaSerLeuGluTyrGlnPhe 174
         |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
Db      646 AAGAAATGGAGACAGAGACCGCTCCCTGGAAATACCAAGTTC 687
    
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Search completed: November 18, 2002, 17:12:32
Job time : 1939 secs

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2